

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop
><MW: 38192, pI: 4.53, NX(S/T): 2
MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCRGRGLVDKFNQGMVD TAKKNFGGNTAWEEKTL SKYSESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQKSEYPD LFEWFVCVKTLKVC CSPGT YGPDCLACQGGSQRPCSG
NGHCSGDGSRQDGS CRCHMGYQG PLCTDCMDGYFSSLRNETHS ICTACDESKTCSGLTNRD CGECEVGWVLDE
GACVDVDECAAEPPPCSA AQFCKNANGSYTCECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLA EKT
CVRKNENCYNTPGSYVCVCPDGFEE TEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

[illegible]

CAGGTCCAAC TGCACTCGGTTCTATCGATTGAATTC CCGGGGATCCTCTAGAGATCCCTC
GACCTCGACACCGCTCGCCAGCGGAGGCGAGCGCCAGCGGCTCTAAAGCGGAAACA
CGCCTGCTGAGGAGCTCGAGCGCAGGAGATCTGACGCGCCGTTTCGTAGTGTGCG
GCACGAGGAGTTTTCGGGCAGCGAGGAGTCTTGAGCAGC **ATG**CGCCCGGAGGAGCGCCTTC
CCTGCCGCGCGCTCTGGCTCTGGAGCATCCTCTGTGCTGCTGCCACCTGCGGGCGAGGCG
CGCCGCGCGCAGGAGGAGAGCTGTATCTTGGATCGATGCTTCAACAGGCAAGAGTATCTCA
TAGGATTTGAAGAAGATATCCTGATTGTTTCAGGGGAAAATGGCACCTTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCATGAATTTTAC
CTGGCAAGCTCGAGGCGAGGACAATCTCTATGAATTCCTGCTCGCTCGCTCCCTGTGATA
AAGGCATCATGCGAGATCAACCGTCAATGTTCCCTCTGTCTGGGAACAGTGCCTCACAGGCA
TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAAAAAGGATGGGTGGCAGCTTTGAAGT
GGATGTGATTGTTTGAATTTCTGAAGGCAACACATTCTTCAAAACCTCAAAATGCTATCT
TCTTTAAAACATGTCAACAGCTGAGTGGCCGAGCGGTGCCGAAATGGAGGCTTTTGTGAAT
GAAGACGCATCTCGCAGTGTCTCTATGTTGGTTCCAGCGACTCACTGTGAGAAAGCCCTTG
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCACTTGCCCACTG
GATTTCTATGAGTGAACTGTGACAAGGAAACCTGCTCAACACCTGCTTTAATGGAGGACC
TGTTTCTACCTCGGAAATGATTTTGGCTTCAGGACTAGAGGAGAGCAGTGTGAATCAG
CAAAATGCCCAACCTCTGCGAAATGGAGGTTAAATGCATTGGTAAAAGCAAAATGTAAGTGT
CCAAAGGTTACCAAGGAGACCTCTGTTTCAAGCGCTGTCTGCGAGCTGGCTGTGGTGCAAT
GGAACCTGCCATGAACCAACAAATGGCCAAATGCAAGAAAGTTGGCATGGAAGACACTGCA
TAAAGGTTACCAAGCCGCTCATACATGCCCTTCAAGGCCAGCAGCGCCCACTCAGGCAG
ACACGCTTCAAGTTAAAAGGCCGAGGAGCGCGGGGACCTCGAATCCAATTAATCACTTG
TGAACTCCGACATCTGAAACGTTTAAAGTTACACCAAGTTCATAGCCTTTGTTAACCTTTCA
TGTTGTGAATTTCAAAATAATGTTATTACCATCACTTAAGATACTGGCCTGAATTTTATTAGCT
TCATTATAAATCTCAGTGTGATATTTACTCTCCTTTAAGTTTCTTAAGTACGTCTGTAG
CATGATGGTATAGATTTTCTTGTTTCAGTGCTTTGGGACAGATTTTATATTTATGTCAATTGA
TCAGGTTAAAAATTTTCAGTGTGATTTGGCAGATATTTTCAAAATTAACATGCAATTTATGGT
GTCCTGGGGCAGGGGAACATCAGAAAGGTTAAATTTGGGCAAAATGCGTAAGTACAAGAAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTTTCAGATTTTATTGTGAGATATTTAGAT
GTTTGTTCATTTTAAAAATGCTCTTAATTTTAAACTCTCAATCAATATATTTTGACC
TTACCTTATTCAGAGATTCAAGTATAAAAAAATAAATAACATCTGGTATGGCATTT
AAACAAATATAATATTTCTAAACCAATGAATAAGGGAATATAATGTATGAACATTTTTCAT
TGGCTTGAAGCAATATAATATATTGTAAACAAACACAGCTCTTACCTATAAACATTTTAT
ACTGTTTGTATGTATAAAATAAAGGTGCTGCTTTTGGTAAATAAATAAATAAATAA
AAAAAATAAATAAATAAAGGCGCGCGCACTTAGAGTCGACCTCGACAGCTTGGC
CGCATGGCCCACTTGTTTATTGACGTTTAAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLLSLRLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPPGGC
RNGGFCNERRICECPDGFHGHCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCTFYPGKCICPPGLEGEQCEISKCPQPCRNGGKICGSKCKCSKGYQGDLCSPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAEERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGGCGTCCGGCGGTTCGCAGAGCCAGGAGCGGAGGCGCGCGGCCAGCCTGGG
 CCCCAGCCACACCTTCACAGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC
 TGCTGTGTGCTGCCGTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGGCGCCGG
 GAGCTAGCACCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGTACTGCCAGGA
 GCAGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCCTACCTTGGGCGCCATCT
 GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACCTTCTGGGACTTC
 TGCCTCGGCGTGGCACCCCTTTTCCCGCGATCCAAGGATGTATGCATGGAGGTCGTATCTA
 TCCAGTCTTGGGAACGTACTGGGACAACTGTAACCGTTGCACCTGCCAGGAGAACAGGCACT
 GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
 GAACCACAGCGCCTTCTGGGGCATGACCCCTGGATTGAGGGGCATTTCGCTACCGCCTGGGCACCA
 TCCGCCCCATCTTCTCGGTGCATGAACATGCATGAAATTTATACAGTGTGAACCCAGGGGAG
 GTGCTTCCACAGCCTTCGAGGCCTCTGAGAAGTGGCCCAACCTGATTCATGAGCCTCTTGA
 CCAAGGCAACTGTGACGGCTCCTGGGCCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
 CAATCCATTCTCTGGGACACATGACGCCTGTCTGTGCGCCCAAGCCTGTCTGTCTGTGAC
 ACCCACCAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTCG
 CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCC
 CTGCGCCCCCTGTATGATGACACAGCCGAGCCATGGGTCTGGGGCAAGCGCCAGGCCACTGCC
 CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCT
 CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
 TGGAGGTGCATGAGGACTTCTTCTTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
 CTGGGAGGCCAGAGAGATACCGCCGCGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
 AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCTGGGGCC
 CAGCCTGGGGCGAGAGGGGCCACTTCCGCACTCGTGGCGGCGCTCAATGAGTGCACATCGAG
 AGCTTCGTGTGGGCGTCTGGGGCCGCGTGGGCAATGGAGACATGGGTCTCACTGAGGCTG
 CGGGCACCAAGCGGGGTCCGGCCTGGGATCCAGGCTAAGGGCCGGCGGAAGAGGGCCCCAATG
 GGGCGGTGACCCAGCCTCGCCCGACAGAGCCCGGGCGCAGGCGGGCGCCAGGGCGCTAAT
 CCCGGCGCGGTTCCGCTGACGACGCGCCCGCTGGGAGCGCGGGCAGGCGAGACTGGCG
 GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGGCCTGGCCTGGGAAGAGCACAGCTGCAG
 ATCCCAGGCCTCTGGCGCCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
 CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTAGACAGGGTCTTGCTCG
 TTGCCCAGGTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCCGACTCCTGGGTTC
 AGTGACCCCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCAACACACCTGGC
 TAATTTTGTATTTTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCGAAC
 CCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCCAAAGTGTGGGATTGCAGGCATGAGCC
 ACTGCACCCAGCCCTGTATTCTTATTCTTCAGATATTATTCTTTTCACTGTTTTAAAA
 TAAACCAAGTATTGATAAAAAAAA

000445 071201
 102120 307000

FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPPIQGCMHGGRIYPVLGTIYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

2000年12月26日

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCATTCTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCCTGTCTTTNGCCCCAGAACCTGTCTGTCTGTACACCCAC
CAGCAGCAGGGCTGCGCGNGTGGGCGTCTCGATGGTGCTGGTGGTTCTTGCCTGCGCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTCTGGGGCAAGCGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCTTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAAGTGCCTGGATGACTCACAGGACTACTACGTGGGCAAGAAGAATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCCTGGTTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCACCCCTGACCCCTCCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCCTCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGCAGGCACTCAGGAGGGCCAGTAAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTTCGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

FIGURE 9

MTHRTTTWARTSRAVTPTCATPAGPMPCSRLLPSSLRCSLHSACSGDPASYRLWGAPLQPT
LGVVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHDPDPMALSRTPTRQISSDT
DPPADGPSNPLCCCFHGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGGAGCCGCCCGCCTGCTGCCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACCTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAAACCTTACAGCAGGACCACTGGCAAGCA
CGTGCAAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGGAAGCCCAGCGGGAAGAGCAAAGACTG
CGTGTTACGGAGATCGTGCTGGAGAACTATACGGCCTTCCAGAACGCCCCGGCACGAGG
GCTGTTTCATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCGAGGCCCACTTCATCAAGCGCCTTACCAAGGCCAGCTGCCCTTCCCCAACCCAGC
CGAGAAGCAGAAGCAGTTTCAGATTGTGGGCTCCGCCCCACCCGCCGACCAAGCGCACAC
GGCGGCCCCAGCCCTCACGTAGTCTGGGAGGCAGGGGGCAGCAGCCCTGGGCCGCCCTCCC
CACCCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCCTGAGGGCCGCGAAGCATCCGAGCCCCAGCTGGGAAGGGGCAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTACACCTGATCTCAGGCCACCAGCCTCTGCGCGCCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTGAGCGACTGAAGGCCTTGACAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCAACTCCTCCTGGCTAGACTGTA
GGAAGGCACTTTTGTGTTGTTGTTGTTTCAGGAAAAAAGAAAGGAGAGAGAGGAAAAATAG
AGGGTTGTCCACTCCTCACATTCACGACCCAGGCCTGCACCCACCCCCAACTCCAGCCC
CGGAATAAAACCATTTTCTCTGC

FIGURE 11

MGAARLLPNLTLCLQLLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGLIGKPSGKSKDCVFTEIVLENNYTAFQ¹NARHEGWMAFTRQGRPRQASRSRQ²NQREAHFIKRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

THE

ACTTGGCCATCACCTGTGGCCAGTGTGGAAAAAATTCTCCCTGTTGAATTTTTTGCACATGGAG
 CACAGCAGCAAAAGAGGGCAACACAGGCTGTGAAGACCGAGACAGCAGGGAGATTTATTAC
 GATACGCCCTCAGAGACTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGACCCCATCAAGT
 CATTTTGATTTTGCTGTTAATTTTTTTTTTTTTTTTTTTTTTCCCAACCATATGTTATTTTAT
 TTTCCGTAATTCAGAAATGGGCTCAGACCAACAAGGTGGCCAGCCATGGGCTTTTTCTT
 GAAGTCTTGGCTTTATCAATTTCCCTGGGGCTCTACTCAGAGGTGCCAAACTCTGTGGCTGCC
 CTAGTGTGTGGCCCTCGCAGCAGGAACCTTGTCTACTGTAATGAGCGAAGCTTGACCTCAGTG
 CCTCTTGGGATCCCGGAGGGGCTAACCGTACTTACCTTCCACAACAACCAATTAATAATG
 TGGATTTCTGTGAGAAGTGCACAAATGTACAGTCCGGTGCACACGGTCTACCTGTATGGCAA
 AACTGGAGCAATTTCCCATGAACCTTCCCAAGAAATGTACAGTTCTTCATTTTGCAGGAAAAC
 AATATTGACACCAATTCACGGGCTGCTCTTGGCCAGTCTTGAAGCTTGAAGAGCTGCACCT
 GGATGACAACTCCATATCCACAGTGGGGGTGGAAGACGGGGCTCTCCGGGAGGCTATTAGCC
 TCAAATTTGTTGTTTTGTTCTAAGAATCACCTGAGCAGTGTGGCTTGTGGGCTTCTGTGGAC
 TTCCAAGAGCTGAGAGTGGATGGAATCGAATTCGCTGTATATCCGACATGGCCTTCCAGAA
 TCTCACAGAGCTTGGAGCGTCTTAATGTGGACGGGAACCTCTGCACCAACAAGGGTATCGCCG
 AGGCAACCTTCAGCCACTTACCAGGCTCTACCAAGTCAAGAAATTTCAAATGTACGTAATTCGCTGTCC
 CACCCTCCTCCCGATCTCCAGGTTACGCATCTGTATCAGGCTCTATTTTGCAGGACAACCGAT
 AAACCAACATTCCTTTGCTAGCCTCTCAAATCTGCGTAAGCTGGAAACCGGTGATATATCCA
 ACAACCAACTCCGGATGCTGACTCAAGGGTTTTTGATAATCTTCCAACCTGAAGCAGCTC
 ACTGCTCGGAATTAACCTTTGGCTTTGTGACTCGATATTAATAGGGTACAGAAATGGCTCA
 ATATATCCCTTCATCTCAACCTGCGGGTTTCATGTGCCAAGCTCTGAACACCTCCGGG
 GGATGGCCGTGAGGAAATTAATATGAATCTTTTGTCTGTGCCACACGACCCCGGCTGT
 CCTCTCTTCCACCCCGCCCAAGTACAGCTTCTCCAGCACCTCAGCCTCCACCTCTCTAT
 TCCAAACCTGACAGAGCTTACACGGCTCCAATCTCTACACATCGAAATTTCCACAGATT
 CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTTCTGAAACGGATCCAGCTCTCTATC
 CATTTTGTGAATGATATCTCAATCAAGTCAAGTGGCTCTCTCTCTACCGTGATGGCAAT
 CAACATCGACATGGGTGAAATGGGCCAAGTTTGTATAGGGGCACTGTTGAGGACGCAATG
 TGACGGGTGGAAGACAACCTAGCCTGGTTAACTCTAGAGCCCGGATCCACCTATCCGATT
 TGTTTGTGTCCTCGGATGCTTTTAACTACCTCGCGGTAGAAGACCAATTTGTTACAGGC
 CACCACCCATGCCTCTATCTGAACAACCGCAGCAACACAGCGTCCAGCCATGACGACAGCA
 CGTCCCAACAGCATATGGCTCCCCCTTTCTGCTCGCGGGCTTGATCGGGGCGCGGTGATATTT
 GTGCTGTGGTCTTTGCTCAGGCTCTTTTGTCTGGATATGCACAAAAGGGGCGCTACACCT
 CCAGAAGTGAATAACAACCGGGGCGCGCGGAAGATGATTATTGCTGAGGCGAGCAACAAGA
 AGGACAACCTCCATCTCGGATGACAGAAACCAAGTTTTCAGATCGCTCTCTTAAATAACGAT
 CAACCTCTTAAGGAGATTTACAGCTGCAGCCATTTACACCCCAATAGGGGCTATTAATTA
 CACAGACTGCCATATCCCCCAACAACATCGCATACGCAACAGCAGCGTGCAGACCTGGAGC
 ACTGCGATACCTGAACCCCAAGGCCAGGCTTACAGGCGGACCAATAGACTCTTGAGAA
 CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
 TTGTGCTATTTGAATATCTGTAATTTTACAGGTGACTATATATAGGATTTAAAAAAGTG
 CTATCTTTCTATATCTCAAGTTAATTACACAGCTTTTGTAACTCTTGCTTTTAAATCTT

FIGURE 13

MGLQTTKWPESHGAFFLKSGLIISLGLYSQVSKLLACPSVCRNRFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLKLLELHLDNISITVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKLKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGQPEQVRGMAVRELNMNLLSCPTTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPITPDWDGRERVTPPISERIQLSIHFVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRYAVEDTICSEATTHASYLNNGSNTASSHEQTTSMSGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRTYSQKWKYNRGRKKDDYCEAGTKKDNSILEMTETSFQIVISLNNQQLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

2010年10月10日 星期六

ACTCTGGAGCAAGCGCGCGCGCGGAGACAGAGGCGAGAGCGAGAAGCTTGGGGCTTCGCTCTCGCTCTCCAAGAGCG
ATCCCGAGAGAGCGCGCGCCCTTCGGCGAGCGGAGAGGCGCAGAGGAAGCCGCGGTGCTGCGCCCTGCC
TCGCTTCCCAGGCGCCGCGCGCTTCGAGCTTGGCCCTTTCGTTCGCTCTGAAATATGGAAAGATCTCGCGAGCT
GCTTTTCTGCTGATCTTCGGACAGAGCTGCTCTCTGCTTCCGCGAGCGAGGAGCGGTCACGTGGAGAGTCCATCT
CTAGGGGCGACGACGCTTCGAGACCCACCGCAGACCTCCCTCTCGAGAGTTCCTGTGAGAACAGAGCGGACACC
TGGTTTTCATCATTCAGAGCTTCGCGAGCTTCAACACCATGATCATATGCAAAAGTTCAGGAGTTCATCGTGGACA
CTTTGCAATTTCTGGACATTTGGTCTCTGATGTCCACCGATGGGCGTCTCTCAAGTATAGGAGCTCTCAAGATAG
AGTTTCTCCCTCAAGACCTCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCTCTCAAGAGGATTCGGGATCTGCTCAACG
GCACCATGATCGGCTGGCCATCCAGTAACTGCTTGAACATCGCATCTCAGAGAGCAGAGGGGGCCGCGCCCTGA
GGGAGAATTTGCCACCGGTCATAATGATGTGCAGATGGGAGACCTCAGGACTCTCGTGGCGAGGTGGCTGCTA
AGGACGGGACACGGGATCTTAATCTTTTGGCATTTGGTGTGGGCGAGGTAGACTTCAACACTTTGAAGTCATTG
GGAATGCGCCCATGAGGACCATGCTTCTCTTTGGCCAAATTCAGCCAGATTCAGACGCTGAACTCCGTTGTCC
AAGAAGAATTTGTGACGGGCCCATCTTCCTGCGACGACCTCTGAGACATAACTTGTGCCAATTTCTGCAACAACTCTG
GCTCATAGCTTCGAGGTGCAAAACAGGCTACATTTCTGAATTCGGATTCAGACGATTCGCAAGATCCAGAGTCTGT
GTGCGATCGAGGAGACCAACTGTGAGGACCTCTTGTGTGAATGTGCGGGCTCCTTCGTCTTCGCAAGTCTACAGT
GCTACGCGCTTGGTGTGAGGATGGGAAGAGGTTGTGGCTTGGACTACTTGCCTCAAGAAACACCGAGATGTGAAC
ATGAGTGTGTAATTTGCTGTATGGCTCTTAACTTTTGCGAGTGGCATGAAGATTTGCTCTTAACCAAGATGAAGAAA
CGTGCAACAGGATCAACTACTGTGCATGAAACAAACCGGCTGTGAGCATGAGTGGCTCAACTGAGAGGAGCTCT
ACTATGCTGCGCTGCCACCTGGTGTCACTCTGGAACCCATGGCAAAACCTCGACGGCTGTGCAACTGTGCAC
AGCAGGACCATGCTGTGAGCAGCTGTGTCTGCAACAGGGAAGTTCTCTTCGCTGCTCAGTGTCTGGAATACTCT
TCATCAACAGGAGGACCTCAGAGCTGCTCCGGGCTGGATTTCTGCTGTAGTACCATGGTTCATGAGGAGCTTCT
GTGTCACTAGGACAGTACTCTTTGGCTTCAGTGTCTTGAGGGACACGTGCTCCGCGAGCATGGGAAGAGTGT
CAAAATTTGAGACTTTGTGCTCTTGGGGGACCAAGTTGTGAACATTCGTGTGAAGCGATGAGATTTCTGTTGT
GCCAGTCTTTGAAGTTTATATATCTTCGCGAAGATGGAAAAACCTCGCAAGGGAAAGATGTCTGCAAGTCTATAG
ACATGGTGTGTGACAACTTTGTGTGAACAGTGAAGTCTATACAGCTCGGAGTCTTGAGGAGGATTCGCGGTCT
CTGAGGATGGGAACGCTCGCGAAGGAAGATCTCTGCAAAATCAACCCACCATGCTCGCAACATTTTGTGTTA
ATATGGGAATTTCTACATTCGAAATCTCAGAGGATTTGTTCTAGTCTGAGGACGGGAAGCGTGTGCAAGAAAT
GCACTGAAGGCGCAATTCAGCTGTGCTTTGTGATCTCTAGCTAGGATTCAGAGTCTTGGAAGAGAATTTTGAAGTGT
TGAGAGCACTTTGTCACTGAAATATAGATTTCTTGCAATTTCCCCAAGCGCGCTCGAGTGGGGTCTGCTGAGT
ATTCCACACAGTCCGACAGATTTCACTCTGAGAAATCTTCAACTCAGCGAAAGACATGAAGAAAGTGGTGGCC
ACATGAATATCGGGAAGGGCTTATGCTGGGCTGGCCCTGAAACACATGTTTGAAGAGATTTTATCCAAAG
GGAAGGGGCGAGCGCCCTTTCCACAGAGGTGCGCAGAGCAGCATTTGTGTACCGAGCGAGCGGCTCAGGATG
ACGTCTTCGAGTGGGCGATAAGACCAAGGCAACATGGTATCATCTATGTATGTGTTGGGTTAGGAAGAAGCCATGT
AGGAGAGACTACAGAGATTTGCTCTCTGAGCGCCAAACCAAGCATCTCTTATGTGCGAAGATCTCAGCAACATGT
ATGAGTAAAGTGAAGAACTCAAGAAAGGCATCTGTGAAGCTCTTAGAAGACTTCGATGGGAACAGGACTCTCAG
ACGGGACATGCCAAAGCGTCCACAGCCAAACGAATCTGAGCGACTCACCATAAATATCAAGAACCTACTTCT
CTGTGTTTAATTTTTCAGTGTGAGTCTGTTTGAAGAAAGCACTTTCTTACGTTCTACACAAAGCTTT
CCCATTTCAACAAACCTTTCAGAGAGCCCTTTGAGGAAAAACACGATCAATGTCAAAATGTGAATCTTATAATGT
TCGAAAGCTTGCACACAGAGGATTAAGAAATTAACACAGCGCTTAGAAGAAATGACACAGAGAAATGGAAGCCC
TGGAAGCTCCGCTGAGATACAGATGAAGATTAAGAAATCGGACACATTTGTAGTCAATGTATACAGGATTAACA
GAACCACTGCGAGCGCCAAAGCTCAGGTCATTTGTAATACAAATGTTGTGAGTAAATACATCAGTACATGTA
GAAACTCGTTTGGCAGCAACAGACAGGAAGTATACCTAACTTGTGTAAATTTTATAGGAAATAAATCTCT
TCAGAAATTCAGAGTAATTTTACAGGTGAGAAATGAATAGTATTCGAAAGTATTTTGAATATACCTGTGGACAC
AATCTGCTTTGCTCATCTCTGCTCTTAAGTGTGAATCTTTAGTACATACATAAGATTTGACAGTCTACTTCT
CTGTAGAACCTGGCCATGAGAAATCTGTTTTTTGTATCGACTTTACCTTGATATATGATATGGATGTATG
CATAAATATCATAGGCATAGTATCTTGTGGAAACAGTTGATTTTATACAAATATTAATATCACCACCTCAG

FIGURE 15

MEKMLAGCFLLLILGQIVLLPAAERERSRGRSISRGRHARTHPTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KRMRLHSLGTGMTGLAIQYALNIAFSEAGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCCTRINICALNKP GC
EHECVNMEESSYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLLI
NEDLKTC SRVDYCLLSDHGCEYS CVNMDRSFACQCPEGHVLSRSDGKTC AKLDS CALGDHGCE
HSCVSSSEDSFVCQCCEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCELEGFRLA
EDGKRCRRKDVCKSTHHGCEHICVNNNGNSYICKCSEGFVLAEDGRRCCKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWAKAKAN
GITMYAVGVGKAIEBELQBIASEPTNKHLYAEDFSTMDIEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTSEFPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSP
EEKHDQCCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTACAGGGCTCGGCTCCCGCGCACGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCCCTGACTCCGTCCCGGCCAGGAGGGC
CATGATTTCCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACTTGCCCGCCAACCGGTGTCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGCGGAGGTGTCTTC
ATCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGGAACCTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGCCCCCTA
CAGCTGTCTCCGTGAATGTGCAAGACAAACAAGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCTCCAGCTCCTCCATCTGCGCTCTCCAGGGTGTGCCCCAT
GTGGGGGCAACGTGACCTTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGACCAGCATTAGATGTATCCGTG
GTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCCTGGTTGGACTGGGGTTGCTGGCTGGGCTGGTCC
TCTGTGACCACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAAATGATATCAAGGAGGATGCC
ATTGCTCCCGGACCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGAAATGGGACCTT
TTCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAGACTGCCACGACAGAT
GGGGCCACCTCTAACCAATATCCCCCATCCCTGGTGGGGTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC
CCCACCACTCATTGGCTAAAGGATTGGGGTCTCTCCTTCTATAAGGGTCACTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCACACTCCTGACCCTTAGTACTCTGCCCCACCTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCTCCTTATGAAGCCAGCTG
CTGAAATTAGTACTACTACCAAGAGTGAGGGGAGAGACTTCCAGTCACTGAGTCTCCAGGC
CCCTTGATCTGTACCCCAACCCCTATCTAACCAACCCCTGGCTCCCATCCAGCTCCCTGT
ATTGATATAACCTGTCAGGCTGGCTTGGTTAGGTTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAATAAATAACATGAAATATGTGTTGTTTTTCATTGCAAATTTAATAAAGATACATAA
TGTTTGTATGAAAAA

0004105.07257

FIGURE 17

MISLPGLVLTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVFFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKGSGPY
SCSVNVQDKQGKSRGHSIKTLELNLVLPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ
WDRQLPSFQTFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTILVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSFRLPTTDGAHPQFISPIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCCTGCGGCCACCGCCAAATGAAACGCCTCCCGCTCCTAGTGGTTTTTTCCACTTTG
TTGAATTGTTCTTACTCAAAATTGCACCAAGACACCTTGTCTCCCAAAATGCAAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGTGCACAA
TTTGTGGAAGATGATAATGAATGTGGAATTTAACTCAGTCCTGTGGCGAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTATCATAATGATGGAACCCGTCTGTATAGAAAATGTGAATGCAAACTGCCATT
TAGATAATGCTCTGTATAGCTGCAAAATATTAATAAACTTTAAACAAAATCAGATCCATAAAA
GAACCTGTGGCTTTGCTACAAGAAGTCTATAGAAAATTTCTGTACAGATCTTTCCACACAGA
TATAATTACATATATAGAAAATATTAGCTGAATCATCTTTCATTACTAGGTTACAAGAACACA
CTATCTCAGCCAAGGACACCCCTTTCTAACTCAACTCTTACTGAATTTGTAAAAACCGTGAAT
AATTTTGTTCAAAGGGATACATTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCC
AAAAGACCACAGAGTTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTTCTTTTTTGAT
TCATATAACATGAAACATATTTCTCCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTTGCATTTTATATTATA
AGAGTATTGGTCTTTGCTTTCATCATCTGACAACTCTTATTGAAACCTCAAATATTGATG
AATTCTGAAGAGGAGGAAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTTATGAACTTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATA
GGTATAGGAGTCTATGTGCAATTTTGGAAATTACTCACCTGATACCATGAATGGCAGCTGTGCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGTGTAAATCACCT
GACACATTTTGCAATTTTGATGTCTCTCTGGTCTTCCATTGGTATTAAAGATTATAATATTC
TTACAAGGTCACCTCAACTAGGAATAATTAATTTCACTGATTTGTCTTGCATATGCATTTTT
ACCTCTCTGGTCTTTCAGTGAAATTCAAAGCACAGGACAACAATTCACAAAATCTTTGCTG
TAGCCTATTCTTGTGTAACCTGTTTTCTTGTGGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTTGCCGAGTCTGTACACTACTCTTTTTTAGCTGCTTTTGCATGGATGTGC
ATTGAAGGCATACATCTCTATCTCATTGTTGTGGGTGTCTATACAAACAGGGATTTTGTGA
CAAGAATTTTTATATCTTTGGCTATCTAAGCCAGCCGCTGTAGTTGGATTTTCGGCAGCAC
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAAACAACCTTTATT
TGGAGTTTTATAGGACCAGCATGCCTAATCATCTTGTTAATCTCTTGGCTTTTGGAGTCAT
CATATACAAAATTTTTCTGTCACACTGCAGGGTTGAAACCAAGAAGTTAGTTGCTTTGAGAACA
TAAGGTCTTGTGCAAGAGGAGCCCTCGCTCTCTGTTCTTCTCGGCACCACTGGATCTTT
GGGGTCTTCCATGTTGTGCACGCATCAGTGGTTACAGCTTACCTCTTCACAGTCAGCAATGC
TTTCCAGGGATGTTTCAATTTTTTATCTCTGTGTGTTTTATCTAGAAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAAAAATGTCCCTGTTGTTTTGGATGTTTAAAGGTAACATAGAGAATG
GTGGATAATTCAACTGCACAAAAATAAAAATTCAGCTGTGGATGACCAATGTATAAAAA
TGACTCATCAAATATCCAATTATTAATACTACTAGACAAAAAGTATTTTAAATCAGTTTTTCT
GTTTATGCTATAGGAATCTAGATAATAAGGTAATAATATGTATCATATAGATATACTATGT
TTTTCTATGTGAATAGTTTCTGTCAAAAATAGTATTGCAGATATTTGGAAAGTAATTTGGTT
CTCAGGAGTGATATCATGTCACCAGGAAAGATTTTCTTTCAACACGAGAAGTATATGAA
TGTCTGAAGGAAACCACTGGCTTGATATTCTGTGACTCGTGGTGGCTTGAACACTAGTCC
CCTACCACCTCGGTAAATGAGCTCCATTACAGAAAGTGAACATAAGAGAATGAAGGGGCAGA
ATATCAAACAGTGAAAGGGGAATGATAAGATGTATTTGAATGAACCTGTTTTTCTGTAGAC
TAGCTGAGAAATTTGTGACATAAAAAATAAGAATGAAGAAACACATTTTACCAATTTTGTGAA
TTGTTCTGAACTTAAATGTCCATAAAACAACTTAGACTTCTGTTTGTCTAAATCTGTTTCTT
TTCTTAATATCTCAAAAAAAAAGGTTTACCTCCACAAATTGAAAAAAA

FIGURE 19

MKRLPLLVPFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSSYYCMCVPGFRSSSNQDRFITNDGTVCIENTVNANCHLDNVCI
NINKTLTKIRSIKEFPVALLQEVYRNSVTDLSPTDIIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTETFEVKTVNNFVQRDTFVVDKLSVNHRRTHLTKLMHTVEQATLRISQSFOKTEFDT
NSTDIALKVFFFDSSYNMKHIIHPHNMMDGDYINIFPKRKAAYDSNGNVAVAFLLYYKSIGPLLS
SSDNFLLPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDYRSLCAF
WNYSPTDMNGSWSSEGCCLTYSNETHTSCRCNHLTHFAILLMSSGPGSIGIKDYNILTRITQLG
IIISLCLAI CIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSTIAGL
LHYFFLAFAWMCI EGIHLYLIVGVVIYNKGFLHKNFYIFGYLSPAVVVVGSAAALGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVLVHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEYYRRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

0603

TGGAAACATATCCTCCTCATATGAATATGGATGGAGACTACATAAATATATTTCCAAAGNG
 AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAAGTTCATTTTTATATTATAAGAGTAT
 TGGTCCCTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAATTATGATAAATCT
 GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTTCAGTCTCAATGAGCTCAAAACCCACCAC
 ATTATATGAACCTTGAAAAATAACATTTACATTAAAGTCATCGAAAGGTCACAGATAGGTATA
 GGAGTCTATGTGGCATTTTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
 GGTCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
 TTTTGCAATTTTGATGTCTCTGGTCCCTTCATTGGTATTTAAAGATTATAATATTTCTTACAA
 GGATCACCACTAGGAATAAATTATTCTCAGTATTTGCTTGGCCATATGCATTTTTACCTTC
 TGGTCTCTTCAGTGAATTTCAAAGCACCGAGA

[illegible]

GCTCCCAAGCAAGAACCTCGGGGCGGCTGCGCGGTGGGGAGGAGTTCGCCGAAACCCGGGCCG
 CTAAGCGAGGCGCTCTCTCCCGCAGATCGCAACGCGCTGGGCGGGGTCAACCCGGCTGGGA
 CAAGAAGCCGCGCGCTGCTGCTCGCGGCGGGGAGGGGGCTGGGGCTGGGCGCGGAGCGGCG
 GGTGTGATGGTGGGTGTGTGCGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCCGG
 TGTCTTTGGGCACTTACCCGTGGGGCCCGTAAGGCGCTACTATATAAGGCTGCCGCCGGAG
 CCCGCGCGCGCTCAGAGCAGGAGCGCTGCGTCAAGGATTAGAGGCCAGCATCCCAACCC
 GGCATCTCAGCGCCGCGCAGCGATCCCGGTGCGCGCCAGGCTCCCGCACCCCTCATCGCCG
 AGCTGCGCGAGAGGCCCAGGAGGTGCGCATGGAGCGGGTGTGTGGTGTCTCACGTATGG
 ATCCTGGCCGGCTCTGGCTGGCCGTGGCGGGGCCCTCGGCTTTCGGACGCGGGGCC
 CCACCTGCATCAAGCTGGGGCGGCAACCCATCCGCTCGGCGACTGTGTACACCTCGGCGCCCC
 ACGGGCTCTTCAGCTGCTTCTCTGCGATCCGTGCGCAGCGCGTGTGGACTGTGCGCGGGCG
 CAGAGCGCGCATAGTTTGTGTGAGATCAAGGCAGTGCCTCTGCGGACCGTGGCCATCAAGGG
 CGTGCAACAGCGTGGCGGTCTCTGTCATGGGCGCGCAGCGCAAGATGACGAGGTGTCTCAAGT
 ACTCGGAGGAAGACTGTGCTTCTGAGGAGGAGATCCGCCAGATGGCTACAGTGTGTACCGA
 TCCGAGAAGCAGCGCCCTCCCGTCTCTCTGAGCAGTGCACAAAGCAGGCGCATGTACAAGAA
 CAGAGGCTTTTCTCCACTCTCTCATTTCTGTCGCCATGCTGCCCATGGTCCAGAGGAGCGTG
 AGGACCTCAGGGGCGCATTTGAATCTGACATGTTCTCTTCGCCCCGGAGACCGCAGCATG
 GACCATTTTGGGCTTGTCAACCGGACTGGAGGCGGTGAGAGTCCCACTTTGAGAAGTAAT
 GAGACCATCGCCCGGCTCTTCACTGCTGCCAGGGCTGTGTTAGTCTGACGCTGGGGGACG
 TGCTTCTACAAGAACAGTCTTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
 GTTGTACATATTAGAGTTTTCATTTGGCAGTGCAGTTTCTTAGCACAATAGACTGTCTGAT
 CATAACATTGTAAGCTGTAGACTTGCCACAGTGTGCTGTGGGCCCCATTTGCTCTCTCGA
 GTTTGTGTGACAAGCTGTGCACTGTCTGATCTGCTTGTAATCACTTCCATTCGATGGGGAAC
 TCACTTCTTTTGAAGAAATCTTATGTCAAGCTGAAATTTCTTAATTTTCTCATCACTTC
 CCCAGGAGCAGCCAGAAGCAGGCGAGTAGTTTAAATTCAGGAACAGGTGATCCACTGTGA
 AAAACAGCAGGTAAATTTCACTCAACCCATGTGGGAATTGATCTATATCTCTACTTCCAGG
 ACATTTTGCCCTTCCAAATCCTCCAGGCAGACTGACTGGAGCAGCATGGCCACG
 GCTTCAGGAGTAGGSGAAGCCTGGAGCCCACTCCAGCCCTGGGACAACTTGAGAATTTCCCC
 CTGAGGCCACTCTGCTCATGTAGTGTGCTCTGAGAATAACTTGTCTGTCCCGGTGTCACTGCT
 TTCATCTCCGAGCCGACAGCCCTTGCCCACTCATAGCTCCCCATGGATTTGGGCGCT
 CCCAGGCCCCCCACTTATGTCAACCTGCACTTCTTGTTCAAAAATCAGGAAGAAGAAAGAT
 TTGAAGACCCCAAGTCTTGTCAAATAGTGTGTGTGGAAGCAGCGGGGAAGACCTAGAAC
 CCTTTCAGCAGCACTTGGTTTTCCAAATGATTTTATGAGTAATTTATTTTGATATGTACA
 TCTCTTATTTTCTTACATATTATATGCCCCAAATATATTATGTATGTAAAGTGAGGTTTG
 TTTTGTATATTAATTTGGAGTTTGGTTTGT

FIGURE 22

M R S G C V V V H V W I L A G L W L A V A G R P L A F S D A G P H V H Y G W G D P I R L R H L Y T S G P H G L S S C F L R I
R A D G V V D C A R G Q S A H S L L E I K A V A L R T V A I K G V H S V R Y L C M G A D G K M Q G L L Q Y S E E D C A F E E
E I R P D G Y N V Y R S E K H R L P V S L S S A K Q R Q L Y K N R G F L P L S H F L P M L P M V P E E P E D L R G H L E S D
M F S S P L E T D S M D P F G L V T G L E A V R S P S F E K

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNL EED
TVTLEVLVAPAVPSCCEVPSSALSGTVVELRCQDKBGNPAPEYTWFKDGIRLLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN SVGYRRCPGKRMQVDDL NISGIIAAVVVVA
LVISVCGLGVCYAQRKGYFSKETSFQKSNSSSKAT TMSENVQWLTPVIPALWKAAAGSGRQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

0000435-07364
123205340660

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
 AAAGAAGAGGAAGATGTTGGGCAACATTTATTTAAACATGCTCCACAGCCCGGACCCTGGCAT
 CATGCTGCTATTCTCTGCAAACTACTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA
 ATGAATTACTCAAATCTCTATGACCATCTATACATACCTCCACCTTCAAAGAATACATCAATA
 TTATATCATTAAAGAAATAGTAACCTTCTCTTCCAAATAGCATGACATTTTGGACAATG
 CAATTGTGGCACTGGCACTTATTTAGTGAAAGAAAACTTTGTGGTTCTATGGCATTTCATCA
 TTTGACAAATGCAAGCATCTTCTTATCAATCAGCTCCTATTGAACCTTACTAGCACTGACTG
 TGGAAATCCTTAAGGGCCATTACATTTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCAAT
 CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
 TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCCTTGGTTTACACCCAGATCCATTAT
 ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACTTTCCAGCCAGATTGCC
 AGCTAACACACAGATTCTTCTCCTACAGACTAACAAATATTGCAAAAATTGAATACTCCACAG
 ACTTTCCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTTATCTTCAGTCACCAAT
 ATTAATGTAAAAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAAAACAACCTTACTGA
 ACTGCCGTGAAAAATGTCGTGCGAACTGAGCAACTTACAAGAACTATATTAATCACAACT
 TGCCTTCTACAATTTGCTGGAGCCTTTATTGGCCTACATAACTCTTCTTCAGCTTCACTC
 AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTTGTATGCTCTTCCAAATCTAGAGAT
 TCTGATGATTGGGGAAAACTCAATTTACAGAAATCAAGACATGAACCTTAAAGCCTCTTATCA
 ATCTTTCGACGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCTTGGTT
 GGACTGAAAACTTAGAAAGCATCTCTTTTACGATAACAGGCTTATTAAGTACCCCATGT
 TGCTCTTCAAAAAGTTGTAATCTCAAATTTTGGATCTAAATAAAAAATCCTATTAATAGAA
 TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGAGATAAATAATAGCCT
 GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTTAAGAAAAATAGAAGC
 TACTAACACCCTAGATTGTCTTACATTCAACCCCAATGCATTTTTCAGACTCCCAAGCTGG
 AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
 CCAAACTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCATCCGTTG
 GATGAACATGAACAAAAACAACATTGATTTCATGGAGCCAGATTCACCTGTTTTCGCTGGACC
 CACCTGAATTCGAAGGTGAGAATGTTGCGCAAGTGCATTTTCAGGGACATGATGGAATTTGT
 CTCCTCTTATAGCTCCTGAGAGCTTTCCTTCTAATCTAAATGTAGAAGCTGGGAGCTATGT
 TTCCTTTCACTGTAGAGCTACTGCAGAACCACAGCCTGAAATCTACTGGATAAACACCTTCTG
 GTCAAAAACCTTTGCGCTAATACCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAACTA
 GATATAAATGGCGTAACTCCCAAAGAGGGGTTTATATACTTGTATAGCACTAACCTTAGT
 TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTCCACAAGATAACAATG
 GCTCTTTGAATATTAATAAGAGATATTGAGGCCAATTCAGTTTGGTGTCTTGGAAAGCA
 AGTTCTAAAAATCTCAAATCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAATTTCTCA
 TGCTGCGCAAGTGTCTGAATACCATCTGATGTCAAGGTATATAATCTTACTCACTGTAATC
 CATCAACTGAGTATAAAATTTGTATTGATATTCACCACTCTACAGAAAAACAGAAAAAAA
 TGTGTAATGTCAACACCAAAGGTTTGCACCCTGATCAAAAAGAGTATGAAAAGATAATAC
 CACAACACTTTATGGCCTGTCTTGGAGGCCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
 GCTGCTCTCTCGCAAAATGAACTGTGATGGTGGACACAGCTATGTGAGTAATTTACTACAG
 AAACCAACCTTTGCATTAGGTGAGCTTTATCCTCCTCTGATAAATCTCTGGGAAGCAGGAAA
 AGAAAAAGTACATCACTGAAAGTAAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT
AAAAACCAACAGGAACCTACTCCAAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLLVQAVDKKVDPCPLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQLTNNIAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTPELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSLVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVVNLFKFLDLNKNPINRIRRGDFSNNMLHLKELGINNMPELISIDSLAVDNLDP
LRKIEATNNPRLSYIHNPNAFFRLPKLESLMLNSNALSAHYGTIESLPNLKEISIHSPNIRC
DCVIRWMNMNKTNIREFMEPDSLFCVDPPPEFQGNVRQVHFRDMMEICPLIAPESFSPSNLNV
EAGSYVSFHCRAETAEFQPEIYWITPSGQKLLENTLTDKIFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFFV
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLGIIGVICLISCLSPENNCDDGGHSYVRNYLQKPTFALGELYPPPLIN
LWEAGKEKSTSLKVKATVIGLPINMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

0607

CCCGGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTTGGAGTAGATGAGGAATGGGCTCTGTATTATGCTGACATTCAGCAATGAATCT
GGTAGACCTGTGGTTAAACCGGTTCCCTCTCCATGTGTCTCCTCTACAAAGTTTTGTTCTTTA
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTTCTTCTCTGGG
GGTTTAAATGTCACCTGTAGCAATGCAAACTCTCAAGGAAATACCTAGAGATCTTCTCTCTGA
AACAGCTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTTAAGG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGACAGCTCGGACTTGTCCGCAATTCCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAAACCCTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTTGGCTGGTTCATATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAAACTGACTGTCTATTGAGAAAGAAAGAAA
GTAGTTTGCgATTGCAGTAGAAAATAAGTGGTTTACTTCTCCCATCCATTGTAACATTTGAA
ACTTTGTATTTcAGTTTTTTTTTGAATTATGCCACTGCTGAACTTTTTAACAAACACTACAACA
TAAATAATTGTAGTTTTAGGTGATCCACCCCTTAATTGTATCCCCGATGGTATATTCTTGAGT
AAGCTACTACTGTAAACATTAGTGTAGATCCATCTCACTATTTAATAGCGAATTTATTTTTTT
AATTTAAAGCAATAAAAGCTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAAAAAAAC

FIGURE 28

MNLVDLWLTRSLSMCLLLQS FVLMILCFHSASMC PKGCLCSSSGGLNVTC SNANLKEI PRDL
PPETVLLYLD SNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGV AETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVIC KTSVLDEHAGRPFL
NAANDADLCNL PKKTTDYAMLVTMFGWFTMVISYVVYVVRQNQEDARRHLEYLKS LPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCAGCCCCCTCCTGGCCTGCTGGCAGCCCATCCTCCTGCTGGTGCT
GGGCTCAGTGCTGTTCAGGCTCGGCCACGGGCTGCCCGCCCCGTGCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCGAGGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACC GCATCAAAACGCTCAACCAGGACGAGTTCGCCAG
CTTCCCGCACTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCCGTGGAGCCCCGGCG
CCTTCAACAACCTCTTCAACCTCCGGACGCTGGGTCTCCGCAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAACAAAGAT
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTCACC CGCCTTCAGCGGCCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCACCTGCACGGCCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAAC
TGCCCTACAGGCCTCAACCTGACGTCCCTGTCCATCAACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCCCTCAACCTCTCCTACAACCCCATCA
GCACCAATTGAGGGTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCCTCCCGCGGCTCAACTACCTGCGCGTGCTCAA
TGCTCTGGCAACAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCCTGCGACTGTCCGGCTCTGTGGGTGTTCCGG
CGCCGTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCGAGTTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCCACTACTTCACTGCGCCCGCG
CCCGCATCCCGGACCGCAAGGCCAGCAGGTGTTTGTGAGCAGGGGCCACACGGTGCACTTT
GTGTGCCGGGCGGATGGCGACCCGCGCCCGCATCCTCTGGCTCTCACC CCGAAAGCACTT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAAACGGCACGTACCTGTGCATCGCGGCCAACCGGGCGGCAACGAC
TCCATGCCCGCCCACTGCATGTGCGCAGCTACTCGCCGACTTGGCCCCATCAGCCCAACAA
GACCTTCGCTTTCATCTCCAACGACCGGGCGAGGGAGAGGCCAACAGCACCCCGCGCCACTG
TGCTTTCCCTTCGACATCAAGACCCCTCATCATCGCCACCACCATGGGCTTCATCTCTTTC
CTGGGCGTCTCTCTTCTGCTGGTGCTGCTGTTTCTCTGGAGCCGGGGCAAGGGCAACAC
AAAGCAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAAGGCATCAGTCCGCCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCGGGCGGGGGGAGGACCCCGG
GGCGGCGGGCAGGGGAAGGGGCTGGTGCACCTGCTCACTCTCCAGTCTTCCCACTC
CTCCCTACCCTTCTACACAGTCTCTCTTTCTCCCTCCCGCTCCGTCCCCTGCTGCCCCCG
CCAGCCCTCACCACCTGCCCTCCTTCTACCAGGACCTCAGAAGCCAGACTGGGGACCCCA
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCGGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACTTGGGTTTCAATAATTATGGATT
TATGAAAACTTGAAATAATAAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLDLLGKNRIKTLNQDEFASFPHLEELNENIVSAVEPGAFNNLFLNRLTL
GLRSNRLLKLIPLGVFTGLSNLTQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGNLSEQLTLEKCNLTSTIPTALSHLHGLIVLRRLHNLINAIIRDYSFKRLYRLKVLEISH
WPLYDTMTFNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMHLHL
LRLQEIQLVGGQLAVVEPYAFRGLNLYLRVLNVSGNQLTTLLEESVFHSGVGNLETLILDSNPLA
CDCRLLWVFRRLWRLNFRQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGPPAILWLSPRKHLVSAKSNGRLTVPFDGTLVRYAQVQDNGTYL
CIAANAGGNDMPAHLHVRSYS PDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFIISFLGVVFLCLVLLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

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00000425 01303

Signal sequence:

Transmembrane domain:

N-glycosylation site.

Casein kinase II phosphorylation site.

N-myristoylation site.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCTTTTCTTCTCCTTTCTGCTG
 CTTCCGGACATTGGAGCACTAAATGAACCTTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
 TTACTTTGTGATGAGATCGGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
 GCTGGAGACGCTCTCTTTGTTTGGCCGTGGAACGTTACAGGGGACCTTTGCAAAAGAGAAGA
 TCTGTTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
 AGTCTGACGGTTTTCAGTGCGCCGCACTTCCAGTTTACCATTATTTCTGATGGCAATTTC
 CCTCAGTCGACTTTTCCCTAAATGAGTTTCGCTAACTTTTATAATGCGGTTAGTTGCAATGG
 AAAACAATGGCTTGATGGAATCGTTCCGGGGCTTTTCTGGGGCTCAGCTGGTGAAAAGG
 CTGCACATCAACAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
 TCTGGAATATCTCCAGGCTGATTTTAATTTATTACGAGATATAGACCCGGGGGCTTCCAGG
 ACTTGAACAAGCTGGAGGTGCTCATTTTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
 GTGTTCCAGTATGTGCCATCACCCACCTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
 CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCCT
 GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAAACATTCCAAAGAATGCC
 CTGATCGGCCGAGTGGTCTGCGAAGCCCCACCAGACTGCAAGGTAAAGACCTCAATGAAAC
 ACCGAAACAGGACTTGTGTCCTTTGAAAAACCGAGTGGATTCTAGTCTCCCGCGCCCCCTG
 CCCAAGAAGAGACCTTTTGCTCTGACCCCTGCCAACTCCTTTCAAGACAATGGGCAAGAG
 GATCATGCCACACCAAGGCTGTCTCCAAACGAGGATACAAAGATCCAGGCAACTGGGAGAT
 CAAAATCAGACCCACAGCAGCGATAGCGACGGGTAGCTCCAGGAACAACACCTTAGCTAAACA
 GTTTACCTGCCCCTGGGGGCTGAGCTGCGACCACATCCAGGCTCGGGTTTAAAGATGAAC
 TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCCAAGCTCTCTAACCTGCAAGGA
 GCTTTTCTACGAGATAACAAGATCCACAGCATCCGAAAACTGCACCTTTTGGATTGACAAAGA
 ACCTCATTTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACCAACACTTTCAAG
 AACCTTTTGGACCTCAGGTGGGTATACATGGATAGCAATTACCTGGACACGCTGTCCCGGGA
 GAAATTCGCGGGGCTGCAAAACCTAGAGTACCTGAACTGGAGTACAACGCTATCCAGCTCA
 TCCTCCCGGGCACTTTCAATGCCATGCCAAACTGAGGATCCTCATTTCTCAACAACAACCTG
 CTGAGGTCCCTGCCTGTGGACGTGTTTCGCTGGGGTCTCGCTCTCTAAACTCAGCCTGCACAA
 CAATTACTTATGTACCTCCCGGTGGCAGGGGTGCTGGACAGTTAACCTCCATCATCCAGA
 TAGACCTCCACGGAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTTCAAGCAGTGGGCA
 GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGTTGAACCTCTT
 TAGAAAGGATTTCAATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
 CGCCCAGTTAACTTCGACAGTAAAAACAGCATGGGTTGGCGAGACCCGGGACGCACTCC
 AACTCCTACCTAGACACCAGCAGGGGTGTCCATCTCGGTGTTGGTCCCGGGACTGCTGCTGGT
 GTTTGTACCTCCGCCCTCACCGTGGTGGGCACTGCTCGTGTATCTGAGGAACCGAAAGC
 GTCTCAAGAGACGAGATGCCAACTCCTCGCGTCCGAGATTAATCCCTACAGACAGCTGTG
 GACTCTTCTTACTTGGCACAATGGGCCCTTACACGCAGATGGGGCCACAGAGTGTATGACTG
 TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGGCAGAGGGAAGGGC
 ATACATCTCTTCCCCACCGCAGCACCCCGGGGCTGGAGGGCGCTGTACCCAAATCCCGCG
 CCATCAGCCTGGATGGGCAATAAGTAGATAAATAACTGTGAGCTCGCACAACCGAAAGGGCCT
 GACCCCTTACTTAGCTCCTCTCTTGAACAAGAGCAGACTGTGGAGAGCTGGGAGAGCGCA
 GCCAGCTCGCTCTTTGCTGAGAGCCCCCTTTTGACAGAAAGCCAGCAGCAGCCCTGCTGGAAG
 AACTGACAGTGCCCTCGGCCCTCGGCCCGGGGCTGTGGGGTTGGATGCCGCGGTTCTATAC
 ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTCCCTTTGGATTAG
 CCCCCTGATGGCTCCTGTGGCTACGCAGGATGGGAGTTGCACGAAGGCATGAATGTAT
 TGTAAATAAGTAACCTTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPT SQFYH
LFLHGNSLTRLPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLLEVLILNDNLISTLPANVFQYVPI THLDLRG
NRLKTLPTYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENI PKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLETPPFKTINGQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANS LCPGGCSCDHIPGSGLKMN CNNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNL LLDLRWLYMDSNY
LDTLSREKFAGLQNL EYLNVEYNAIQ LILPGTFNAMPKLRILILNNNLLRSLPVDVVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGPNWECSC TIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHSNSYLDTSRVSISVL
VPGLLLVFVTSFTVVGMLVFILNRNRKRSKRDRANDSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577, 608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349, 354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTTGACCCCGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGCGGCTAAGGGAAACTGTTGGC
CGCTGGGCCCGCGGGGGGATTCTTGGCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCTCGAGCGGGACAGATCCAAAGTTGGGAGCAGCTCTGCGTGCGGGGCCTCAG
AGAATGAGGGCCGGCGTTGCGCCTGTGCCTCCTCTGGCAGGCGCTCTGGCCCGGGCCGGGCGG
CGGCGAACACCCCACTGCCGACCGTGTGCTGCTGCGGCTCGGGGGCCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCGAGGCGGCCGAGGAGGCTGCATCTCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCGGGCGCCAGCTGCGCGCTGTGCTGCGCGCTCTGCGGGCAGGCCCAGG
GCCCGGAGGGGGCTCCAAGACCTGTGTTCTGGTTCGCACTGGAGCGCAGGCGTTCCCACT
GCACCTGGAGAACGAGCCTTTGCGGGGTTCTCCTGGCTGTCTCCGACCCCGCGGCTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCCGCGCGAGATGCGC
GGTACTCCAGGCCACCGGTGGGGTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAGTTTGAGGTCTTGTGTCTGCGCCGCGCCCCGGG
GCCGCTCTAACTTTAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTGTCCCTGCCCC
GGGAGGTACCTCGGTGCTGGCAAAATGCGCAGAGCTCCCTAACTGCGCTAGACGACTTGGGAGG
CTTTGCTTGCAGATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCCGCTCTTGTGTGACCA
GTGGGGAAGGACAGCCGACCTTGGGGGGACCGGGGTGCCACCAGGCGCCCGCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCCAATCAGGGTCGACGAGAAGCTGGGAGAGAC
ACCCTTTGCTCCCTGAACAAGACAATTAGTAACATCTATTCCTGAGATTCTCGATGGGGAT
CACAGAGCAGATGTCTACCCCTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGATTCCAAGTTAAATCTACGACTTCTCTGCCACTCCTCAGGCTTT
CGACTCCTCCTCTGCGGTGGTCTTTCATATTTGTGAGCACAGCAGTAGTAGTGTGGTGATCT
TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTACAGAAAGCCCTCTCTCCAGCCA
AGGAAGGAGTCTATGGGCCCGCGGGCCTGGAGAGTGATCCTGAGCCCGTGCTTTGGGCTC
CAGTTCTGCACATGTGACAAACAATGGGTGAAAGTCCGGGACTGTGATCTGCGGGACAGAG
CAGAGGGTGCTTGTGCGGAGTCCCTCTTGGCTCTAGTGATGCATAGGGAACAGGGGA
CATGGGCATCCTGTGAACAGTTTTTTCACTTTTGATGAAACGGGGAACCAAGAGGAATTAC
TTGTGTAACAGCAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGGAAGTGCCCTTAGGA
TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTCGGAGAA
TTTGGAGAAGTGATTGAACTTTCAAGACATGGAAAACAAATAGAACACAAATATAATTACA
TTAAAAAATAATTCTACCAAAATGGAAAAGGAATGTTCTATGTTGTTAGGCTAGGAGTAT
ATTGGTTGCAATCCCAGGGAATAAATAAAAAATTAAGGATTGTTGAT

0004406 07430

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRSCVTS GEGQPTLGGTGVPTRRPFATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTSSATPQAFDSSSAVVFI FVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEFAALGSSSAHCTNNGVKVGDCLDRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTTCAGCAGTGGCCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
 CGTCGAGTCAGACGGCACCATAATCGCCCTTTAAAGTGCCTCCGCCCTGCCGGCCGCGTATC
 CCCCAGGCTACCTGGGCGGCCCGCGCGGTGCGCGCTGAGAGGGAGCGCGCGGCAGCCGA
 GCGCCGCTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGGTGGGTGCGGA
 GGGCGTGTGTGCGCGCGCGCGCCGTGGGGTGCAAAACCCGAGCGTCTACGCTGCCATGA
 GGGGCGCGAACGCTGGGCGCCACTCTGCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
 CAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
 TATTGGCAGTGAAGGTTTTTCTGGAGTGTACCCTCCAATAGCAAATGTACTTGGAAAATCA
 CAGTTCCCGAAGGAAAAGTAGTCGTTCTCAATTTCCGATTTCATAGACCTCGAGAGTGACAAC
 CTGTGCCGCTATGACTTTGTGGATGTGTACAATGGCCATGCCAATGGCCAGCGCATTGGCCG
 CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
 TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
 AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC
 CCCCAACTGGCCAGACCGGGATTACCTGCGAGGAGTCACTTGTGTGTGGCACATTGTAGCCC
 CAAAGAATCAGCTTATAGAATTAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGC
 CGATATGATTATGTGGCTGTGTTTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA
 GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTTCTTATTCAGT
 TTTTATCAGACTTAAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTTCAGGCCAAAA
 AAACTGCCTACAACCTACAGAACAGCCTGTCAACCCACATTCCCTGTAACCAACGGGTTTAAA
 ACCCACCCTGGCCCTTGTGTCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
 GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCATCACTCGCGATGGGAGTTTG
 CAGCCACAGTCTCGATCATCAACATCTACAAGAGGGGAAATTTGGCGATTTCAGCAGGCGGG
 CAAGAACATGAGTGCCAGGCTGACTGTGCTCTGCAAGCAGTGCCCTCTCCTCAGAAGAGGTC
 TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCCAAAATCATGCCAAAACAGC
 TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG
 TTAACAGTGAACGTGTGCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTCT
 TCTCAGTAGAAAAAAAATACTTTATAAAATTACATATTCTGAAAGAGGATTCGAAAAGATGG
 GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAGTTCTT
 TGCCTGCTGTCAAGGAGCAGCTATCTGATTGGAACCTGCCGACTTAGTGCGGTGATAGGA
 AGCTAAAAGTGTCAAGCGTTGACAGCTTGAAGCGTTTTATTTATACATCTCTGTAAAAGGAT
 ATTTTGAATTTAGTTGTGTGAAGATGTCAAAAAAAGATTTTAGAAGTGCAATATTTATAGT
 GTTATTGTGTTTACCTTCAAGCCTTTGCCCTGAGGTGTTACAACTCTGTCTTGCCTTTTCTA
 AATCAATGCTTAATAAAATATTTTTAAAGGAAAAA

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FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVLNFRFIDLESDNLCRYDFVDVYNHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAPNERGQYCGGLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSTADGFIGHYIFRPKKLPTTTEQPVTTFPVTITGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITITITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTGCGTTCTT
 CCTTCTCCGTGGCCTACGAGGGTCCCCAGCCTGGGTAAAGATGGCCCCATGGCCCCGAAGG
 GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCAGGACCTATCTGG
 CTCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCCGCCTCAGCCCCATCCGTGTCATACCTG
 CCGGGGACTGGTTGACAGCTTTAACAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG
 GTGGAAACACTGCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCGCTG
 GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCCTGCTGGAGCT
 GAGTGAGGAGCTGTTGGAGAGCTGGTGGTTTCAACAGCAGCAGGAGGCCCGGACCTCTTCC
 AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCCGAGGCACCTTCGGGCCCTCCTGC
 CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
 GACACGAGGGGGCAGCGGGCAGTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
 AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
 TTTGGCCCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAAGTGTGTCGAATGCAAGAAGGG
 CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAAC
 GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
 GCCTGCCTAGGCTGCATGGGGCAGGGCCAGGTGCTGTAAGAAGGTAGCCCTGGCTATCA
 GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
 ACAAGCAGTGTGAAAAACCCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
 ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
 AGAAGACGAGTTGGTGGTGTGTCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
 CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
 ACTGGCTACTGGTTGTGACAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
 ATCGCGGCCACCACTGTAGGACCTCCTCCCACCCACGCTGCCCCAGAGCTTGGGCTGCC
 TCCTGTGAGCACTCAGGACAGCTTGGTTTATTTTGGAGAGTGGGGTAAGCACCCCTACCTG
 CCTTACAGAGCAGCCAGGTATCCAGGCCCGGGCAGACAAGGCCCCTGGGGTAAAAAGTAGC
 CCTGAAGGTGGATACCATGAGCTCTTACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
 ATTTCAAAAGTTTTCTTAATGGTGGCTGCTAGAGCTTTGGCCCCCTGCTTAGGATTAGGTG
 GTCCTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCTCTGT
 TCTGTGTTCAACCATCCCCACACCCATTGCCACTTATTATTATCTCAGGAAATAAAGA
 AAGTCTTGAAAGTTAAAAA

FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGNTAWEEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKCCPAGTFGPSCLPCPGGTERPCGGYGQCEGEGTRGSGHCDQAG
YGGACGQCGLGYFEARNASHLVCSACFGPCARCSGPESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTBGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTDELVVLLQQMFPG
IITCALATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACCTCTGGGTGTTGCCCTTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
GCCCACCTTGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCACGTCGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGGAAAGAGGTTTCAGCCAGAGC
TTCGAGAGAGTGGCCCGCAGGTTCTTGGCGTTGGAGGCCAGCACACCTGCTGGTGTTCGG
CATGGAGCAGCGGCTGCCGCCCAACAGCGAGCTGGTGACAGGCCGTGCTGCGGCTCTTCCAGG
AGCCCGTCCCCAAGGCCGCGCTGCACAGGCACGGGCGGCTGTCCCCGCGCAGCGCCCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCACGAGAGCGGCTGGAAGGCCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGTCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCCAAGCTGGTCCGCTTTGCCCTCGCAGGGGGG
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCTTGACCTTGGGGACTATGGAG
CTCAGGCGACTGTGACCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTCAAGTGGC
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATAGCGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTCGAGGGTACCAGGAGAGCTG
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTCTCTAGTGAGCCCTGAATTTGCTT
CCTCTGACAAAGTTACCTCACCTAATTTTGCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
GAGCCCTTGCTCAGTTTTCTCTATTCTATTATTCACTGCACTATATTCTAAGCACTTACAT
GTGGAGATACTGTAACTGAGGGCAGAAAGCCCCANTGTGTCAATTGTTTACTTGTCTGTAC
TGGATCTGGGCTAAAGTCTCCACCACCACCTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAAACATGAATAAAACATTTTATTCT
AAAA

FIGURE 42

MQPLWLWCALWVLPASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQS FREVAGRFLALEASTHLLVFGMEQRLPPNSLVQAVLRRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLG DYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEALAFKWP
LGPQRCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSASD GALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

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GTCTGTTCCCAAGGAGTCTCTCGGCGGCTGTTGTGTCACTGGCCTGATCGCGATGCGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCTCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACCTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCTGTGCTACTCGGGCTTTTCTTCTCCCCGTGTGGAGTGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACCTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCCTCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCACGAATCCCAAAGCACCCGTGCCTTCAGCAACTCTTCTATGTCTCT
GAATCCCAACAACAGAGAGCTGGTCTTTGATCCCCGTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGCGACCGAATGGGTATGGGACACCCATGACTTCAAATGTGTCGCGCATGGAAGAT
GTGGAGCGGAATGTGGGGGTCTATCGTGGCAGCGCTCCTTTGTAACCTGTATTCTCTCGGGAT
CTTGTTTTTTGGCATCTGGTTTGCTATAGCCGAGGCCACTTTGACAGAACAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTCGGTGTGACCCCTGGTCCGGCTACCGCCTATCATCTGCATTTGCCCTTACT
CAGGTGCTACCGGACTCTGGCCCCCTGATGTCTGTAGTTTACAGGATGCCTATTATTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTGACGTATGTGCCCC
ATCCTCCTTCATGCCCTCCCTCCCTTCTTACCCTGCTGAGTGGCCTGGAACTTGTTTTAA
GTGTTTATTCCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGTGCGAGGAATCTGCACCTCAACTGCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGTTTCTGGGCTCTTTCTTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCTCTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCCAGAGGCTGAGGCAAGCGGATACCTTGAGTGGGAGTTCGGGATCAGCCTGACCA
ACATGGAGAAACCTCTACGGAATACAAAGTTAGCCAGGCATGGTGGTCATGCTCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAATCCAGCTCAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLS CAYSGFSSPRVEW
KFDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYYTCMVSEEGNSYGEVKV
KLIVLVPPSKPTVNI PSSATIGNRAVLTCSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGT PMT SNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYS SRGHFDR TKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCGCGCCGAGCCCGCTTCCACCCGACCTCTGCCAGGCGCAGGCCCCAGCTCAG
GCTCGTGCCACCCACCAAGTTCAGTGCCGCACCAAGTGCGCTTATGCGTGCCCTCACCTGG
CGCTGCACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCCTGCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCAGCGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAAACCAATGAGATCCTCCCGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCTCTGTGGGAATGCCACATCCTC
CTGTCCCGAGAGCCAGTCTGGAAGCCCACTGCCCTATGGGGTTATTGCAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTACCGGCCACCCTCCTCCTTTTGTCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGTGCTGTGCAGAACAGAAGAC
CTCGCTGCCCTTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACCTGCCACAGCCAGAAGTGA
GGGCTGGCCCCAGGCAGCTCCAGGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLLDCSDGSDEEBCRIEPTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
RNC SRLACLAGE LRCTLSDDCIPLTWRC DGH PDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTS LRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLV TATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTS LP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGCAGCAGAGGTGCGGCACAGATGCGG
GTTAGACTGGCGGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTTCTAGAGCAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCCGGCATTCCCAGAAATGGCTTCAGGACCCCGAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTTCAC'TGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAAGAGACTGTGTTGAAGCATTTTAATGGAACCTAGGCTGGATCCCAAGTGA
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTGATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGCATGAAGGATTCAAGATCCGG
TACCCGACCTACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCC
CATCTGTCGAAGGTGCCCTGAGACCTTAGCCCTCTTCTAATGGCTATGTAACATCTCTGAGC
TCCAGACCTCCTTCCCGGTGGGGACTGTGATCTCCTATCGCTGCTTCCCGGATTTAAACTT
GATGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCACCCCGGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGTCT
GCCACCGCGGCCCTTGTGAGCGCTACAACCACGGAAGTGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAAGTGTGCTGCTGCTGCTGCTGCTGCTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTCCCCCAGGGGGCCTCCCGGAG
TTCCAGCAGTGACCCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTTACCCGTGGACGACAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
CACAGGCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAA
GTCTGTATTACCTCCAGGTGCCAAGAGAGCACCCACCCTGCTTCGGACAACCCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCCCACTGGGT
GTTGTTCTTAAGAAACTGATTGATTAAAAAATTTCCAAAGTGTCTGAAAGTGTCTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCTTTCTCTCTTGGTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAATATGCTATGCTGATAGAGTGGTGGGGCTGGAAGCTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAAAAATTAAGNAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPYSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATATSULLLVLLLVILARMFQTKFAHFPPRGPPRSSSSDPDFVVVD
GVFVMLPSYDEAVSGGLSALGPGYMASVGGQCPLPVDDQSPPAYPGSGDDTDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIISTAEVASTSPGIHHAHWLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCGTGCGGTCCGTGCGGTGGCCTAGAGA
TGCTGCTGCCGCGGTTGCAGTTGTGCGCGACGCTCTGCCCGCCAGCCGCTCCACCGCCGT
AGCGCCCGAGTGTGCGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC
TCGGATTGAGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGGAGGGACACAGAGGCTTGTTA
TAAAGTCATTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCAATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
CACAATTTAGGAACCTGGTATGTGGATGAGCCGTCTGCGGCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAATGATGA
CGGTGCAACATGAAGAACAAATTTCAATTTGCAAATATTTCTGATGAGAAACCAGCAGTTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAAACATTTAAAGAAAGTAGAGAAGCTGCCTTGAATCTGGCCCTACAT
CCTAATCCCCAGCATTTCCCTTTCTCCTCCTCCTTGTGGTCACCACAGCTTGATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCCTCACCAGGGAAAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTATTCCGAGTGTGTT
CGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTTGTGACCAATGACATTTATGA
GTTCTCCCCAGACCAATGGGGAGGAGTAAGGAGTCTGGATGGGTGAAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACAATGGAAGAAGAAATGATAAGCAAAATC
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
GCAGTGATAAGATGGGCTGTGGAGCTTGGAAAACACCTCTGTTTTCTTGCTCTATACAG
CAGCACATATTATCATACAGACAAAAATCCAGAATCTTTTCAAAGCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAAATAAATCAAATAAAGA
GCAGGAAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGTQPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQKLI EKFIENLLPSDGD FWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGEETELTTPVLPEETQEEDAKKTFKESREAALNLAYILIPSIPLLLLIV
VTVVVCVWWICRKRKREQDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSES G FVTILVSVESGFVTNDIYEFS PDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAEIQEADGQCPVDRSLLKLKMVQVVFRRHGAR
SPLKPLPLEBEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMPAGQL
TKVGMQQMFPALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPILIHTEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKVKVDRMGIDSSDKVD
FFILLDNVAEEQAHNLPSCPMLKRFRARMIEQRAVDTSLYIILPKEDRESLQMAVGPFHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMS VYTLSPKEYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACTTCACCTGCCTTGGTCAATGGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCTCTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACCGTGTGTGATG
ACGGCTGGGACATTAAAGGACGTGGCTGTGTGTGTGCCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAGATACATTGGCTCAGTGTGAGCAAGAAGAAGTTTATG
ATTGTTTCACATGATGAAGATGCTGGGGCATCGTGTGAGAACCCAGAGAGCTCTTTCTCCCCA
GTCCAGAGGGGTGT CAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGGAAAGTGAA
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAGGTGG
TGTGCCGCGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
GGATTGCCCTTCTGGGCCTTGGGGGAAGAACCTTGCAACCATGATGAAGACACGTGGGTGCG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAAC TGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTTCGTTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTGGGGGTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGCTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAACTACATCA
CCACCTTTCCTATGTCTCCACATTGCACACAGCAGATTC CAGCCTCCATAATTGTGTGTAT
CAACTACTTAAATACATTCTCACACACACACACACACACACACACACACACACATA
CACCATTGTCTCTGTTTCTCTGAAGAACTCTGACAAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAAGATAAATTTCTGAATTTGGTTATGGGGTTTCTGAAATTG
GCTCTAATCTAATTAGATATAAAATTTCTGGTAACTTTATTTACAATAATAAAGATAGCAC
TATGTGTTCAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRVLVGGHLRCEGRVEVEQKGQWGTVCDDGWDIKDVAVLC
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC
ENPESSEFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCTGWSLRAAKVVCRQLGCCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPGWKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGWVGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 56

MDFITSTAILPLLLFGCLGVFGLFRLLQWVRGKAYLRNAVVTGATSGLGKECAKVFYAAGA
KLVLGCRNGGALBELLIRELTASHATKVQTHKPVLVTFDLTDSGAIVAAAAILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDRVMEETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGKMSI
PFRSAYAASKHATQAFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAGVKKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 58

MKFLLDI L L L L L P L L I V C S L E S F V K L F I P K R R K S V T G E I V L I T G A G H G I G R L T A Y E F A K L K S K
L V L W D I N K H G L E E T A A K C K G L G A K V H T F V V D C S N R E D I Y S S A K K V K A E I G D V S I L V N N A G V V
Y T S D L F A T Q D P Q I E K T F E V N V L A H F W T T K A F L P A M T K N N H G H I V T V A S A A G H V S V P F L L A Y C
S S K F A A V G F H K T L T D E L A A L Q I T G V K T T C L C P N F V N T G F I K N P S T S L G P T L E P E E V V N R L M H
G I L T E Q K M I F I P S S I A F L T T L E R I L P E R F L A V L K R K I S V K F D A V I G Y K M K A Q

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCGCGGCTC
AGGGAGGAGACCGACTGCGCCGCAACCTGAGAGATGCGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCCTGTGTATGCTGGCCCCGTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAAGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCAGGACTGAACATGA
AGAGTTATGCGCGCTTCTCACCGTGAATAAGACTTACAACAGCAACCTCTCTCTCGGTTT
TCCCAGCTCAGATACGCCAGAAGATGCCCCAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
AGGTTATCCATGTTTGGACTCTTTGTGGAACATGGGCCTTATGTTGTCAACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAAATCCA
GTGGGCACAGGCTTCAGTTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTTATACAGTGCACTAATTCAGTTTTCAGATATTTCCCTGAATATAAAAATA
ATGACTTTTATGTCACTGGGAGCTTTATGCAGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTTCTGATCCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTTGAGGCCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
AAGTGATCCTTCTTACTTCAGAAATGTTACAGGATGTAGTAATTACTATAACTTTTTCGGGT
GCACGGAACCTGAGGATCAGCTTACTATGTGAATTTTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGGAATCAGACTTTTAATGATGGAACATAGTTGAAAAGTACTTGCAGAG
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAGGATCCAGGAATACAAGAAGGCAGAAAAAAAGTTTGGAAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC
GAGGTGGAGCATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAATCGA
TTCATTTATGGAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCCAAGAGAACAT
CAGAGGTTTTTCATTGCTGAAAAGAAAATCGTAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTTTCATATCTGCAAGATTTTTTTCATCAATAAAAAATTATCCTTGAAACAAGTGAGC
TTTTGTTTTTGGGGGAGATGTTTACTACAAAAATTAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAAATGA
AATTTTAGGGCTTGAAATAGGAAGTTTAAATTTCTTCAAGAGTAAGTGAAGGATGCAAGTTG
TAACAAACAAGGCTGTAACATCTTTTCTGCCAATAACAGAGTTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATGGATAAGAAATAGCTCAATTATCCCAATAAATGGATGAAGCTATAA
TAGTTTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTTAGAACAAAAGAAATCTTTGAAATA
AAAAATTATATATAAAAGTAAAAAATAA

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGSGQLFLTPYIEAGKIQKGRELSL
VGFPFGLNMKSYAGFLT VNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSMNMLRDRDFPWT TTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARLDYSALI QF
FQIFPEYKNNDFVVTGESYAGKYVPAIAHLIHS LNPVREV KINLNGIAIGDGYSDPESIIG
YAEFLYQIGLLDEKQKQYFQKQCHECIEHIRKQNWFEAFEILDKLLDGDLTSDPSYFQNV TG
CSNYYNFLRCTEPEDQLYVVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLR EDTVQSVKPWLT
EIMNNYKVLINQGLDIIVAAALTE RSLMGMDWKGSQ EYKKA EKKVVKIFKSDSEVAGYIRO
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCCAGTCTTGTGGCTACAACAT
 TTTTCCCTTTCTTAACAAGTTCTTAACAGCTGTTCTTAACAGCTAGTGATCAGGGGTTCTTCTT
 GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACCTCAGGGTGACCACTCCTTG
 CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
 TCTAAATAGGAAGGAATTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
 CTGGGGGAGGGCTTGCCTAAACAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
 AAGACGTGCGGGTAGGATAGGGGAAGACTGGGTTTGTCTTAATATCAAAATGACTGGCTGGG
 TGAACCTTCAACAGCCTTTTAACTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
 TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
 GACCAAAATAGATAACAGGATTCCTGAACATTCTTAAGAGGGAGAAAGTATGTTAAAAATA
 GAAAAACCAAAATGCAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGGGGACCTTGGGTC
 AGGCCAGCCTCTTTGCTCCTCCCGAAATTTATTTTGGTCTGACCCTCTGCTTGTGTTTT
 GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACAGGAGCCGTCT
 CCTCACCGCCGCCCTCTCAGCATGGAAACAGAGGCAGCCTGGCCCCGGGCCCTGGAGGTGG
 ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCCAGCAGCCGGC
 ATGCCCTCAGTTCAGCACCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACCTGACCGT
 CCACCAAGGGACGGGGGCCGTCTATGTGGGGCCATCAACCGGCTCTATAAGCTGACAGGCA
 ACCCTGACCATCCAGGTGGCTCATAAGACAGGGCCAGAAGAGCAACAAGTCTCGTTACCCG
 CCCCTCATCGTGACGCCCTGCAGCGAAGTGCTCACCCTCAACCAATGTCAACCAAGCTGCT
 CATCATTGACTACTCTGAGAACCGCTGCTGGCCTGTGGGAGCCTCTACCAGGGGGTCTGCA
 AGCTGCTGCGGCTGGATGACCTCTTCATCCTGGTGGAGCCATCCCAAGAAGGAGCACTAC
 CTGTCCAGTGTCAAACAAGACGGSCACCATGTACGGGGTATTGTGCCCTCTGAGGGTGAGGA
 TGGCAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCCGACCTGTCCA
 GCCGGAAGCTGCCCGAGACCTGAGTCTCAGCCATGCTCGCATGAGCTACACAGCGAT
 TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCTGGCCCTGGTCTCCCACTTTGACAT
 CTTCTACATCTACGGCTTTGTCTAGTGGGGGCTTTGTCTACTTTCTCACTGTCCAGCCCCGAGA
 CCCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTTTCTACACCTCAGCATCGTGGCG
 CTCTGCAAGGATGACCCCAAGTTCCACTCATACTGTCTCCTGCCCCCTGGCTGCACCCGGGC
 CGGGGTGGAATACCGCCTCCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
 AGGCCCTCAATATCACAGCCAGGACGATGTACTCTTTGCCATCTTCTCCAAAGGGCAGAAG
 CAGTATCACCAACCCCGCGATGACTCTGCCCTGTGTGCTTCCCTATCCGGGCCATCAACTT
 GCAGATCAAGGAGCGCTGCGAGTCTTGCTACCAGGGCGAGGCAACCTCGGAGCTCAACTGGC
 TGCTGGGAAGGACGTCCAGTGACAGGAAGGCGCTGTCCCCATCGATGATAACTTCTGTGGA
 CTGGAGATCAACAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCTGTACACCA
 CAGCAGGACCCGATGACCTCTGTGGCCTCTAGCTTTTCAACCGCTACAGCGCTGGTTTTTG
 TGGGACTAAGAGTGGCAAGCTGAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC
 ATTCACTCCTCAGCAAGAGTCCCTCTTGGAAAGGTAGCTATTGGTGGAGATTTAACTATAG
 GCAACTTTATTTCTTGGGGAACAAGGTTGAATGGGGAGGTAAGAAGGGGTTAATTTTGTG
 ACTTAGCTTCTAGTACTTCTCTCAGCCATCAGTCATTGGGTATGTAAAGGAATGCAAGCGTA
 TTTCAATATTTCCAACTTTAAGAAAAAATTTAAGAAGGTACATCTGCAAAAGCAA

FIGURE 62

MGTLGQASLFAPPNGYFWSHDHSAFCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSSRSVLLSVVWVLLAPPAAGMPQFSTFHSNDRDWTFNHLTVHQGTGAVYVGAIRNV
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL
YQGVCKLLRLDDLFIIVPEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLRDPRESSAMLDYELHSDVFSSLIKIPSDTLALVSHFDIFYIYGFASSGGFVYFL
TVQPETPEGVAINSAAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAAQAFNITSQDDVLFALFSGKQKYHHPDDSALCAFPPIRAINLQIKERLQSCYQEGN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTFVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCNSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGCTGAGTGCAGGACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAACACGCGCGATGACCA
 CGTGGAGCCTCCGCGCGAGGCGCGCCCGACGCTGGGACTCCTGCTGCTGGTCTCTTGGGCTCCTCTGGTGTCTCC
 GCAGGCTGCGACTGGAGCACCTTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGCAGGCCAAGGGCTGGA
 ACTTCATGCTGGAGGATTCACACCTTCTGGATCTCTCGGGGCTCCATCCACTATTTCGCTGTGCCCGAGGAGTACT
 GGAGGGACCGCTGCTCGCATGAAGGCTGTGGCTTGAACACCCCTACACACCTATGTTCGCTGGAACTTGCATG
 AGCCAGAAAGAGGCAAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCTTCTGCTGATGGCCGACAGATCG
 GGCTGTGGGTGATTCTCGCTCGAGGCCCTACATCTGCAGTGAGATGGACCTCGGGGGCTTGCACGCTGGCTAC
 TCCAAGACCTGGCATGAGCTGAGGACAACTTACAAGGGCTTCCACGAGCAGCTGGACCTTTATTTTGACCAAC
 TGATGCTCAGGCTGGTGCACCTCCAGTACAAGCGTGGGGGACCTATCATTCGCGTGCAGGTGGAGATGAATATG
 GTTCTTATAAAGAACCCCGCATACATGCCCTACGCTCAAGAAGGCACTGGAGGACCGTGGCATTTGGGAACCTGTC
 TCCTGACTTCAGACAAACAAGGATGGGCTGAGCAAGGGGATTGTCCAGGAGATTGTGGCCACCATCAACTTGCAGT
 CAACACACGAGCTGCAGCTACTGACCACCTTTCTCTTCAACGTCAGGGGACTCAGCCAAAGATGGTATGGAGT
 ACTGGACGGGTGGTTTGAAGCTCTGGGGAGGCCCTACAATATCTTGGATTCTTCTGAGGTTTGGAAACCGTGT
 CTGCCATGTGGAGCGCGCTCCTCCATCAACCTCTACATGTTCCAGGAGGCCAACCTTTGGCTTCATGAATG
 GAGCCATGCACTTCCATGACTACAAGTCAGATGTACCAGCTATGACTATGATGCTGTGCTGACAGAAGCGCGCG
 ATTCACAGGCCAAGTACATGAAGCTTCAGAGCTTCTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
 ACCTTCTTCCCAAGATGCCGATGAGCCCTTAAAGCCAGTCTTGTACCTGTCTCTGTGGGACGCCCTCAAGTACC
 TGGGGGAGCCAATCAAGTCTGAAAAGCCCATCAACATGGAGAACCTGCCAGTCAATGGGGGAAATGACAGTCCCT
 TCGGGTACATTCTCTATGAGACCAAGCATCACCTCGCTCTGGCATCCTCAGTGGCCACCTGCATGATCGGGGGCAGG
 TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGACAAGAGATGCTGTCCCTGATCCAGGGTT
 ACACCGTCTGAGGATCTTGTGTGAGGAATCGTGGGCGAGTCAACTATGGGAGATATTTGATGACCGCAAG
 GCTTAATTGGAATCTCTATCTGAATGATCACCCCTGAAAAAATCTGAGCATCTATAGCTCGGATATGAGAGAGA
 GCTTCTTTTCAGAGGTTTCGCGCTGCGCAAAATGGNGTTCCCTCCGAGAAACACCCCATATACCTGCTTCTCTTGTG
 GTAGCTTGTGACTCAGCTCCACGCTTGTGACACCTTCTGAAGCTGGAGGGCTGGGAGAGGGGGTGTGATTCA
 TCAATGGCCAGAACCTTGGACGTTACTGGAACTTGGACCCGAGAGAGCGCTTACCTCCAGGTCCCTGGTTGA
 CAGCGGAAATCAACAGGTCATCGTTTTTGGAGAGACGATGGCGGGCTCTGCATTAACAGTTACAGGAAACCCCC
 ACCTGGGCGAGGAACAGTACATTAAGTGAAGCGGTGGCACCCCTCTCTGCTGGTGCCAGTGGGAGACTGCCGCTC
 CTCTTGACCTGAAGCCTTGGTGGCTGCTGCCACCCCTCACTGCAAAAGCATCTTCTTAAAGTAGCAACCTCAGGG
 ACTGGGGGCTCAGACTCTGCCCCCTGTCTCAGCTCAAAACCCCTAAGCCTGCGAGGAAAGGTGGGATGGCTCTGGGCC
 TGGCTTTGTGATGATGGCTTTCCTACAGCCCTGCTCTTTGTGCCAGGCTGTGCGGCTCTCTCTAGGGTGGGAGC
 AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGTGAAACGTGCCCTTGACCGGACGTCAACAGCC
 TGCAGCATCTGCTGAGCTCAGCGCTGCTCTTTGTGTTCTCGGGAGGCTTGGCCACATCCCTCATGCGCCCAT
 TTTATCCCGAAATCCTGGGTGTGTACACAGTGTAGAGGGTGGGGAAGGGGTGTCTCACCTGAGCTGACTTTGTT
 CTTCCTTCAACACCTTCTGAGCCTTCTTGGGATTCTGGAAGGAACCTCGGCGTGAGAAACATGTGACTTCCCTT
 TCCTTCCCATCTCGCTCTTCCACAGGGTGAAGGCTGGGCTGGAGAAACAGAAATCTCACCTCGCTCTTCC
 CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGGAGGAGACATGTGAGTCTCGGAGAGGCCATGGCCCATGTCTGCA
 CATCCAGGAGGAGGAGCAGAAAGGCCAGCTCACATGTGAGTCTTGGCAGAGCCATGGCCCATGTCTGCACATCC
 AGGGAGGAGGAGCAGAAAGGCCAGCTCACATGTGAGTCTTGGCAGAGCCATGGCCCATGTCTGCACATCCAGGAGG
 GAGGAGCAGAAAGGCCAGCTCACATGTGAGTCTTGGCAGAGCCATGGCCCATGTCTGCACATCCAGGAGGAGG
 ACAGAAAGGCCAGCTCAGTGGCCCGCTCCACACCCCCACGCCCGAACAGCAGGGGCGAGAGCAGCCCTCTTTC
 GAAGTGTGTCCAGTCCGCACTTGAAGCTTGTCTGGGGCCAGCCCAACACCTTGTGGGCTCAGTGTCTGTA
 GTTCAGTAAAGCTATAACCTTGAATCACAA

CG004435.071207

FIGURE 64

MTTWSLRRRPARTLGLLLLVLGFLVLRRLDWSTLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIHVFRVPREYWRDRLLKMKACGLNTLTITYVPWNLHEPERGKFD FSGNLDLEAFV LMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRRTTYKGFT EAVDLYFDHLSRVVPLQ
YKRGGP IIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVE LLLTSDNKDGLSKGIVQGV L AT
INLQSTHELQ L LTTFLFNVQGTQPKVMMEYWTGWFD SWGGPHNILD S SEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFDYKSDVTSYDYDAVLTEAGDYTA KYMKLRDFFGSISGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGNGQSF GYILYE
TSITSSGILSGHVHDRGQVFVNTV SIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYS LDMKKSFFQRFGLDKWXS L PETPTLP AFFLGSLSIS
STPCD TFLKLEGWEKG VVFINGQNLGRYWNIGPQKTLTYLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
CTGGTGAGGGTTCTTACTTTGGCCTTCGGTGGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGGCTCGGCCCGAGGCCCCAGGACCTCCACTCCCAATGTTGGAGGAATC
CGACACGTTGACGGTCTGTCCGCGCTCTCAGACTAGAGGAGCGCTGTAAACGCCA**ATGG**GTCTCC
AAGAAGCTGTCTGCTCCCTCGTTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGCTTCGTAGTGGATAGGGGTCTAGCCGGTTTCTCCTAGACGGGGCCC
CGTTCCGCTATGTGTTCTGGCAGCCTGCACTACTTTCGGGTACCGCGGGTGCTTTGGGCCGAC
CGGCTTTTGAAGATGCGATGGAGCGGCTCAACGCCATACAGTTTTATGTGCTCTGGAAC
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGCCTTTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCACTAGAGACCAGGACCTTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCTCGTTGCTTCGAAACCTGAAATTCATCTAAGAACCCTC
AGATCCAGACTTCCTTGCCGCGAGTGGACTCTCGTTCAAGGCTTGTCTGCCAAGATATATC
CATGGCTTTATACAATGGGGCAACATCATTAGCATTGAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCATTGGCTGGGGCTCTCCGTGCACCTGCTAGG
AGAAAAGATCTTGCTCTTACCACAGACTGGGCCTGAAGGACTCAAGTGTGGCTCCTCCCGG
GACTCTATACCACGTGATGTTTTGGGCCAGCTGACAACTGACCAAAATCTTTACCTGCTT
CGGAAGTATGAACCCATGGGCCATTGGTAAACTCTGAGTACTACAGGCTGGCTGGATTA
CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTTGGATATTGG
AATGTTGCCGATAAGAAGGGACGCTTCCTTCCGATTACTACAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTTGCTCTTCGAGATGTCATCAGCAAGT
TCCAGGAAGTTCCCTTTGGGACCTTTACCTCCCCGAGCGCCCAAGATGATGCTTTGGACCTGTG
ACTCTGCACCTGGTTGGGCATTTACTGGCTTTCCTAGACTTGCTTTGCCCCCGTGGGCCAT
TCATTTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
GAACCTATATGACCCATACCATTTTTGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC
CATGACCGTGCTATGTGATGTTGGATGGGGTGTTCAGGGGTGTTGTGGAGCGAAATATGAG
AGACAAACTATTTTTGACGGGGAAACTGGGGTCCAAACTGGATATCTTGGTGGAGAACATGG
GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
GGGCAAAACAATCCTTACCAGTGGATGATGTTCCCTCTGAAAATTGATAACCTTGTGAAGTG
GTGGTTTCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTCT
ACTCCAAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
ACCAAGGGCCAAAGTCTGGATCAATGGGTTTAACTTGGGCCGGTACTGGACAAAGCAGGGGCC
ACAACAGACCTCTACGTGCCAAGATTCTGCTGTTTCTAGGGGAGCCCTCAACAAAATTA
CATTGCTGGAACCTAGAAGATGTACCTCTCCAGCCCCAAGTCCAAATTTTGGATAAGCCATC
CTCAATGACCTAGTACTTTGACAGGACACATATCAATTCCTTTGAGCTGATACACTGAG
TGCCCTCTGAACCAATGGAGTTAAGTGGGCACT**GGA**AAGGTAGGCCGGGCATGGTGGCTCATGC
CTGTAACTCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTCTCAAGA
CCAGCCTGGGCCAATGGTGAAACCCGCTCCACTGAAAAATCAAAAATTAGCCGGCGGTG
ATGGTGGGCACCTCTAATCCAGCTACTTGGGAGGCTGAGGCGAGGAAATTGCTTGAATCC
AGGAGGCAGAGTTGCACTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTCAAAAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDGRGHRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLCLKMRWSGLNAIQFYVWPWNYHEFPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGFYI
CAEWEMGGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDPSYMRHLAFLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLRLKYEHPGLVNSEYTTGWLDYWGQNHSTRSVSAVTKGLENMLKGASVNMVMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPLGPLPPSPKMMML
GPVTLHLVLGHLLAFDLCLCPRGPIHSILPMTFEAVKQDGHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNMARDKLFLTGKLGSKLDILVENMGRLSFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWFFPLQLPKWPYPQAPSGPTFYSKTFPILGSGVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLVYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

[illegible]

GCTTTGAACACGCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCCTCTACACTCTCTTCTGGTTATTCCAGGATACCTTTGAAGGAATATT
CTTTGAAAAAGTCAGAGAAGAGAGCAGTTTGTAGTGACATTCCAGATGTCAAAACGATTTT
GCGTTCCTTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTTGGTGTGTT
CTTGTCAGAAGTTAGTGAAAATAAAGTTAGGGAAATTAGTTTGAACCATGAGTGGAACATTG
AAAAACTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
CTGTGCGGGGTGCCCGATGCTGTCTTTGACCTCAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGTCTAAGATTTCTCAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTTCTTCGCGATCACTTGAGA
TGCCTTCACGTTGAAGTTCACTGATGTGGCTGAAATTCCTGCTCGGTGTATTTGCTCAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACTCTGAAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTTCTCCAGCTGAAGACCAATTTGACCAAAGTT
CCCTCCACATTACAGATGTGGCTCCACCTTTACAAGAGTTAGTCTCATATGACGGCAC
TAAACTCTGGTACTGAACACGCTTAAGAAATGATGAATGTGCTGAGCTGGAATCCAGAG
ACTGTGAGCTAGAGGAATCCCACTGCTATTTTTCAGCCTCTCTAATTTACAGGAACCTGGAT
TTAAAGTCCAATAACATTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAACAGACT
GACTTGTTTTAAATATTGGCATAACAAAATTGTTACTATTCTCCCTCTATTACCCATGTCA
AAAACCTGGAGTCACTTTATTTCTTAACAACAAGCTCGAATCCTTACCAGTGGCAGTATTT
AGTTTACAGAAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTTCCAATAGA
AATAGGATTGCTTCAGAACTGCAGCATTTCGATATCACTGGGAACAAGTGACATTCTGC
CAAAACAATGTTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGAGCTGAAGGGGAACCTG
CTTGGAACCGCTGCCAGCCAGCTGGGCCAGTGTGCGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTTGATACCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCTTTGCAAAATGGGATTTAAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTTGTAGGGTTTTAAGTCATTCATTTCCAATCATTTTTTTTTTTCTTTGGGG
AAGGGGAAGGAAAAATTATAACTCATTAATCTGGTCTTTTTTAAATGTTTGTAACTTGGAT
GCTGCCGCTACTGAATGTTTTACAAATGCTTGCTGCTAAAGTAATGATTAAATTGACATT
TTCTTACTAAAAAATAAAAA

FIGURE 68

MAYMLKKLLISYISIIICVYGFIGLYTLFWLFRIPLKEYSFEKVVRESSFSDDIPDVKNDFAFLLHMVDQYDQLYSKRFGVFLSEVSENKLRISLNHEWTFEKLQHI SRNAQDKQELHLFMLSGLVPDAVFDLTDLVDLKLLEIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMIGLESRLRLHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCLELIPHAIFSLSNLQELDLKSNNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESPLPAVVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKRLTLNLGQNCITSLPEKVGQLSQLTQLELKGNCCLDRPLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIPFANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

[illegible]

CCACGCGCTGCGGGCCTCTCTCTCGGACCTTGGCACTTTCACATCTCTCTTTATTCAGCAAACTGACTTTTTTATTTCTCT
TTTTCCTTCATCTCTGGGCGACGTGGGAGCTCTAGGCCCTCTGGGAGACATTTGTGTTTTACACATACGAT
CTGTGTTGGGGTTTCTTCTCTCTCCCTCAGTACATGGCATCTTGAAGTGGTTGTGTGGGAGGGAGACACGTTGG
CGTCAGTGGTCTGCTTGCTCATTTATCGCTCTAGGTACATCGAAGTCTTTGAACTCCATACAGTGAATATGCTCGT
ATCGCTGTGTATCTCTGCGGCCCTTGCTCTCTGCTATGATGTGTGCTGCTCTGTCTCTTCAAAATACACAAC
GCGCTAAAGCTCGAAAGAACTCGAAGCTGTGGCTGTAAAAAATACAACCCACAGAGTGTGGTGGGCAAG
AACGACCAAGCGCAAAACCATTGCCACGGAGTCTTATCTGCGCTCGAGTGTGTGGAAGATATAGAATGTGTGCC
AGTTTGTGATCTGCGGCCACTTGCTGTTTGGGACATGTAATGAGGGCTCTGAGTATGAAAGAGCTCTCTTCTCA
CGAGAGCGCTGAAGACTCTCAATGATCTCAATGAGGCCACTGTTTGTGATGTGACGACAGAGAAGAGCCACG
CTCCCCCATCAGTTTTCATGAGAAATAATCATGCTGCTGCTGGGAACAGCTGTGTGCGAGATCCCTTACAGAGAGCT
CACTGGGGGCAACCTCTCCAGGAAGAGTTGGGAGAGAGAACCTCATCTGGGGATCTGTGATAAACAGTCA
CAGCATCTGCTCTATTCTACACAAATCATCCCTTCTGCTGGCTGGAAGTACGTTTCTCTGGAGTGTCTCCAGAA
GCTGATGTAAACAGAGGCTCTAAAGACTGTGGCTCTTAAAGCTGCGCAGAGCCTTGCCAAATAGGAGTCTGTA
AGAGAGCTCATGTCATTGACCTCTTAAATCTTCTGTTTGGCGAGGACTGACATAGTGGCGAGTCTGAAGCAAT
CGAAGCTGCACTAGTCTATGGGGTGCCAATATCCGACAGACAGCAAAAGCATGATCTGCAACTCAATCCC
ATGTGGAAGTCCAGCTGGACATAGAAAGACCAAGAAACAAAGAGCATAGAAATTTCTTCTCTATGTCCAGTGT
GATTCAGATGGAAGCTGTGAAAGTGAAACAAATAAAGTCTTGAAGCAACTCCAGCAATGGGCGCTCTGTAGG
CAAGTCTCGAATAAAAAGCATATGTCCGTGATTTGAATCATCATCAGATACATGAGTTTCAAAATAGTTACT
GACTCAGCAAGATCTCAAGAAGTGTCTTGTCTCTACTACTTCTCTCTTCAACTCTCTATTTCOAAGTCT
GGCGTGTCTCTGGATATCTTGAAGAGTCTCTCACCAGCCCAATTACCCAAGCGCATCTGGTGAAGTGGCTTAT
TGTGTGTGGCACAACAAGTGGAGAAAGTACAAGAATAAACTAAACTTCAAGAGATTTTCTTAGAAATAGAC
AAACAGTGCAAATTTGATTTTCTGTCATATATGATGCCCTCCACAACTCTGGCTGATTTGACAGCAATCTGT
GGCGCTGTGACTCCCACTTCGAATCTGCATCTCAAACTCTGTAGCTGTGTGTGTACAGATATTTGCAAACT
TACCGGGATTTCTCGCTCTCTACACTCAATTTATAGCGAAACATCAACAATCAATCTTAACTTGCTCTCT
GAGGAGTAGAGATTTATTAAGCAAACTACTTAGAGGCTTTTAACTCTAATGGGAATAACTGTGCACTAAAA
GACCCAACTTGACAGCAAAATTTCAATGAATGTGTGAAATTTCTGTGCTCTTAATGGATGTGTGTGACATCA
AAGGTAGAAGTCACTCAATTACTTACAACAATAACCTTTCTGTGATCTCAAACTTGTGAAGTATCAGC
CGCTGAGAAACACTTCAGATTTGTGTGAAGTGTGAAATGGGACATATTTCTACAGTGGAGATAATATACATAAC
GAGATAGTATTAATACAAGTCAAAATGCTGCTGGGCAATAACACAGCATGGCTCTTTTGAATCAATTTCA
TTTGAAGAAGCTATACTTAATCACCAATTTATGTGGATTTGAACAAACTCTTTTGTTCAGTTAGTCTGTGAC
ACCTCAGATCCAAATTTGGTGTGTGTTCTGTATACCTTGAGGCTCTCCCAACTCTGACTTGTGCATCTCAACC
TAGCACTTAATCAAGTGTGAGTGTGATCTCGAGATGAACTTGAAGTGTATCTCCCTTAATTTGGACACTATGGGGA
TCTCAGTTTAAATGCTTTAAATCTTGAGAAGTATGAGCTCTGTGATCTGAGTGTAAAGTTTGAATATGTAT
AGGAGTGACCAACCAAGTCTGCTGTCAATCAAGTGTGTGTCTCCAGAAAGCAACAGACATTTCTCATATAAATGG
AAAAACAGATCCATCATAGAGCAATCTGCTGAAAGAGGATCGAAGTGCAAGTGGCAATTCAGGATTTGACAT
GAAACACATCTCGGAGAAACTCCAAACAGGCTTTTCAACAGTGTGATCTGTTTCTTCACTAGGTTCTAGCTGT
AATGTGGTGACTGTAGCGCAATCAGTGGAGCATTTTGTAAATACAGGCGAGACTCAAAATCCAGAGACTCA
CGAACATCTTAAATACAGTGTCAACCTTAATGAGACATTTTCTTCCAGATGCGAAAGAAATCTACTCTGT
GGCTACACATATATAGATAAATAGGAGGGCTGTGAAGTGTACACAGGCTGCACTGTAAAAAAA

FIGURE 70

MELVRRRLMPLTLLILSCLAELTMAEAEFGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFSYYQLDPDGSCSEENIKVFDGTSSNGPLLGQVCSKNDYVPVFESSSTLT
FQIVTDSARIQRTVFVFFYFFSPNISIPNCGGYLDTLEGSFTSPNYKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDFLAIYDGPSTNSGLIGQVCGRVTPTFESSSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVVIISKYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIIVKCEMGHNST
VEIIYITEDDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNTLTFVQVSLHTSDPN
LVVFLDTCRASPTSDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYKWKTDSSIIGPIRLKRDRSASGNSGFGHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCGAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGCTGCTGC
TGCTGCCCGCGCCGCTGCCCTGCCCAAGCGCCACGCGCTTCGACCCCACTGGGAGTCC
CTGGAGCGCCCGCAGCTGCCCCGCGTGGTTTGACCAGGCCAAGTTCGGCATCTTTCATCCACTG
GGGAGTGTTTTCCGTGCCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCCCTCCTAGTTTCAAATATGAAGAT
TTTGGACCACTATTTCACAGCAAAATTTTTTAATGCCAACCACTGGGCAGATATTTTTCAGGC
CTCTGGTGCCAAATACATTGTCTTAACTTCCAACATCATGAAGGCTTTACCTTGTGGGGGT
CAGAAATATTCGTGGAACCTGGAATGCCATAGATGAGGGGCCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACGAACTGACCTCGGTTTTGGACTGTACTATTCCTTTTTTGA
ATGGTTTTCATCCGCTCTTCTTGGAGATGAATCCAATTCAATCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
TCGGATGGTGACGAGGAGCACCCGATCAATATGGAACAGCACAGGCTTCTTGGCCCTGGT
ATATAATGAAAGCCAGTTTCGGGGCACAGTAGTCACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCAGTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAACCTGCATGACAATAGACAACTGTCTGGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAAATGGTGAAGCAACTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTTGATGAATATGGGCCCACACTAGATGGCACCATTCTGTAGTTTTTGAG
GAGCGACTGAGGCAAGTGGGGTCTGGCTAAAAGTCAATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCAGAAATGACACTGTCAACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTTCTTAAATGGGCCACATCAGGACAGCTGTTCCTTGGCCAT
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG
GATTTCTTTGGAGCAAAATGGCATTATGGTGAAGTGCACAGCTAACCATTCATCAGATGC
CGTGTAATGGGGCTGGGCTTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACTGGATAAGAAAAATTTATTTGGCAGTTTCAGCCCTTTCCTTTTCCCACTA
ATTATATAGTTATGCATCACTTAATATGGGGATATTTTCTGGGAAATGCATTGCTAGTCAAT
TTTTTTTTGTGCCAACATCATAGAGTGATTTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAAAAGTGTAAAAATAAATGGTGCACCTGTATAGGCGACTTACCACGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGCACATTA
TTGAACACTGCCAGAGCTTATAAATACTGTATGCTTAGGCTACACTACATTTATAAAAAAA
GTTTTCTTTCTTCAATTATAAATAACATAAGTGACTGTAACCTTACAAACGTTTTTAATT
TTTAAAACCTTTTTGGCTCTTTTGTAAATAACACTTAGCTTAAAACATAAACTCATTTGTGCAA
ATGTAA

0304035.071301

FIGURE 72

MRPQELPRLAFPLLLLLLLLLPPPPCPAHSATRFDPWTWESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRDRLRFGLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDDGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGNNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTIVPDVWYTSKPEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKGWGALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTTGAGCATCTGCCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTCTTTGCGTGCAGAGAGCT
TTCCATCCAGGTGTCAATGCAGAAATATGGGGATCACCCCTGTGAGCAAAAGGCGAACCAGC
AGCTGAATTTACAGAAAGCTAAGGAGGCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGAGCTATGGCTGGGTTGGAGA
TGGATTCTGGTCTATCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGTTGGGTG
TCCTGATTTGGAAGGTTCCAGTGAGCCGACAGTTTGCAAGCTATTGTTACAACTCATCTGAT
ACTTGGACTAACTCGTGCAATTCAGAAATATCACCACCAAGATCCCATTATTAACACTCA
AACTGCAACACAAACACAGAATTTATTGTCAGTGACAGTACCTACTCGTGGGCATCCCTT
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAATGATTTGTGTCAAGAAATTTTATGAAACTAGCACCATTGTCTACAGAAAC
TGAACCATTTGTTGAAAAATAAGCAGCATTCAGAAATGAAGCTGCTGGGTTTGGAGGTGTC
CCACGGCTCTGCTAGTCTGCTCTCCTCTTCTTTGGTGTGCAAGCTGGTCTTGGATTTTGC
TATGTCAAAAGGTATGTGAAGGCCCTTCCCTTTTACAAACAAGAAATCAGCAGAAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCTTAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAAGAGTCCAAGAGTCCAAGCAAACTACCGTGCAGTGCCTGGAA
GCTGAAGTTTATGATGAGACAGAAATGAGGAGACACCTGAGGCTGGTTCTTTTCATGCTCC
TTACCTTGCCCGAGCTGGGGAATCAAAGGGCCAAAGAACCAAGAAGAAAGTCCACCTT
GGTTCCTAAGTGAATCAGTCAAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAAATGC
CCTTCTCCTTATTGTAACCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAAAGGCCCTCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCGCGAGCTCAGAC
CCTTTCTTCACTCTGAAAGAGAAACACGATATCCCACTGACATGTCTTCTGAGCCCGGTA
AGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTCAAACTTGAG
ACCTAATCTCTGTAAGCTAAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGAGCTGTAAACACAGACAGGGTCAAAGTGTCTCTGAAACATTGAGTTGGA
ATCACTGTTTAGAACACACACACTTACTTTTCTGGTCTTACCCTGCTGATATTTTCTCT
AGGAAATATACTTTTACAAGTAACAAAAATAAAACTCTTATAAATTTCTATTTTCTGTA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTTAAAAAGTAATAAATTC
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGCTGTGCAAGGTATTACACTCTGTAAT
TGAATATTATTTCTCAAAAAATGACATAGTAGAACGCTATCTGGGAAGCTATTTTCTCA
GTTTGTGATTTCTGACTTATCTACTTCCAACTAATTTTATTTTGTGCTGAGACTAATCTT
ATTCAATTTCTCTAATATGGCAACCATTTATAACCTTAATTTTATTATTAACATACCTAAGAAG
TACATTGTTACCTCTATATACCAAGCACATTTTAAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCCTTTTCCAAACAAGAAGGAGCTGAGAGATGCAGAAATATTTTGTGACAAAAAATTA
AGCATTTAGAAAACCTT

030445-07304

FIGURE 74

MARCFSLVLLLLTSIWTTRLLVQGSRLAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGWVGDFVVISRISPNPKCGKNGVGVLWKPVSQRQF
AAYCYNSSDTWTNSCIPEIIITKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAPKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFNTNKNQKEMIETKVVKEEKANDSNPNEESKTKDNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

RECEIVED

Signal sequence:

Transmembrane domain:

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGCGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTG
GGGCCCCAGCCTGGCCCCGGGTACCCCTGGCATGAGGAGATGGGCCCTGTTGCTCCTGGTCCCA
TTGCTCCTGCTGCCCGGCTCCTACGAGCTGCCCTTCTACAACGGCTTCTACTACTCCAACAG
CGCCAAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCTGTTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGCG
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGGCGTGTGCGTGTCAAATGGTGGAAGCT
GTCCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT
TTGGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCAATTGACGGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCCTTACCAGTCCCCCA
ACGGGCGCTACCAAGTTCACCTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG
GTGGCTCCTTTGAGCAGCTCTTCCGGGCCCTGGGAGGAGGGCCTGGACTGGTGCAACGCGGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTGCCCCGGCAGCCCTGCGGTGGCC
CAGGCCTGGCACCTGGCGTGCAGAGCTACGGCCCCCGCCACGCGCCCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCCCAAGGGGCGGGTGTACTACCTGGAGCACCCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATCGCCAAGTGGGAC
AGCTCTTTGCCCGCTGGAAGTTCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCTGTGGTTCACCCGCATCCTAACTGTGGGCCCCCAGAGCCTGGGGT
CCGAAGCTTTGGCTTCCCCGACCCGAGAGCCGCTTGTAACGTTGTTACTGCTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCCTGCCGCATTCCCTCACTGGCTGTGTATTATTAGAGTGGTT
CGTTTTCCCTGTGTGGTTGGAGCCATTTTAACTGTTTTTATACTTCTCAATTTAAATTTTCT
TTAAACATTTTTTACTATTTTTTGTAAAGCAAACAGAACCCAATGCCTCCCTTTGCTCCTG
GATGCCCCACTCCAGGAATCATGCTTGCTCCCCCTGGGCCATTGCGGTTTTGTGGGCTTCTG
GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCCAGAGTGGGC
GGTGGCCTGTCTAGAATGCCGCCGGGAGTCCGGGCATGGTGGGCACAGTCTCCCTGCCCT
CAGCCTGGGGGAAGAAGAGGGCCCTCGGGGGCCCTCGGAGCTGGGCTTTGGGCCCTCTCCTGCC
CACCTTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGGCTAGGCTGGAA
GCCAGTCTTAGGCTTCCAGGCGAAATCTGAGGGAAGGAAGAACTCCCCCTCCCGGTTCCCT
TCCCCCTCTCGGTTCCAAAGAACTGTGTTTTGTGTGTCATTTCTCTGTTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTGTACTTTGGACAATAAATGGTGTATGACTGCCTTCCGCCAA
AA
AA

FIGURE 78

MGLLLLVLPLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYYEPALVSPRRVRVKWWKLSENGAPEKDVLAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRLLHRYDVF CFATALKGRVYYLEHPEKLTLT EAREACQEDDATIAKVGQLFAAWKPHGLDR
CDAGWLADGSVRYFVVHHPNCGPPEPGVRSFGFPDPQSRLYGVICYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCTGCTGC
TTCTGTGTCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGTGCACCAGGCGGGCCCCCTGAGCGACGCTCCCATGATGACGCCACCGGAA
CTTCCAGTACGACCATGAGGCTTTCTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA
CCCCAGAGGAAAGCCAGGCCCGTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGAC
GGCGACGGCTGGGTGTCTGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCCCTGGGACACGTACGACACGGACCGCGACGGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGGTGAAGAATTTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAGATGCTGGCTCGGGACGAGCGGCGTTTCCGGGTGGC
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGG
AGTTCCTCACATGCGGGACATCGTGATTGCTGAAACCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCGGGGACTTCGGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACAGCCC
CTGGTGGAAGCCAACCACTGTGTCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCACGATGAGCTGTGAGCACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAATGACCGGAGGAGGGGCCGCTGTGGTCTGGCCCCCTCCTGTCCAGGCCCCGAGGAG
GCAGATGCAGTCCCAGGCATCCTCTGCCCCCTGGGCTCTCAGGGACCCCTGGGTGCGGCTTC
TGTCCCTGTACACCCCCAACCCAGGGAGGGGCTGTATAGTCCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCCAGCCCAGACCCAGGGACCCCTTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCTT
GGCCCCAGCCCTCTCCTGCCTGGCCTGGCCTGGGACACCTCCTCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLLLRHGAQGKPSPDAGPHGQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKFEDQLTPESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDRDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHWVLPAPQDQPLVEANHLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCCTTGCCCTTCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
 GCGGCGGGCGCGGGTGCAGGGGATCCCTGACGCCCTCTGTCCCTGTTTCTTTGTGCGCTCCAG
 CCTGTCTGTGCTGCTTTTTTGGCGCCCCCGCCTCCCGCGGTGCGGGGTGACACACCGATCCTG
 GGCCTTCGCTCGATTTCGCGCCGAGGCGCCTCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
 CGGGTTCGTCTGTCTCTCTCTCTGCGCCGCGCCCCGGGGATCCGAAGGTTGCGGGGCTCT
 GAGGAGGTGACGCGCGGGGCCCTCCCGACCCCTGGCCTTGCCCGCATTCCTCTCTCCCGAG
 GTGTGAGCAGCCTATCAGTCACCAATGTCGCGAGCCTGGATCCCGGCTCTCGGCCCTCGGTGTG
 TGTCTGCTGCTGCTGCCGGGGCCCGCGGCGCAGCGAGGGAGCCGCTCCCATTTGCTATCACATG
 TTTTACCAGAGGCTTTGGACATCAGGAAAAGAGAAAGCAGATGTCCTCTGCCAGGGGGCTGCC
 CTCTTGAGGAATTCCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
 GCTGCTGTCCACAGGGGAGTAATCAGCAACTCAGGGGGACCTGTACGAGTCTATAGCCTACC
 TGGTCGAGAAAACATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAAATGCTTTCTAGAT
 GGTCTGCTCTTTTACAGTAACATAAGGCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
 GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAAACCCGAGAAGAAAACTGG
 CAATAAAGATTGTAAAGCAGACATTGCATTCTTGATTGATGGAAGCTTTAATATTGGGCAGC
 GCCGATTTAATTTACAGAAGAAATTTTGTGGAAAAAGTGGCTCTAATGTTGGGAATTGGAACA
 GAAGGACCATATGTGGGCCCTTGTTCAGCCAGTGAACATCCCAAAATAGAATTTTACTTGAA
 AAATCTTACATCAGCCAAGATGTTTTGTTTGGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA
 ATTCCAATACAGGAAAAGCCTTGAAGCATACTGCTCAGAAATTTTTCACGGTAGATGCTGGA
 GTAAGAAAAGGGATCCCCAAAGTGGTGGTGGTATTATTATGATGGTTGGCCTTCTGATGACAT
 CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTTATAGTTTCTGTGGCCA
 AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCACATTGTTGACAAGGCTGTCTGT
 CGGAATAATGGCTTCTTCTTACCACATGCCCACTGGTTTGGCACCACAAAATACGTAAA
 GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
 CAGTGAACATTGCCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGGCTC
 ATGCTTGAATTTGTTTCCAACTAGCCAAGACTTTTGAATCTCGGACATTGGTGCCAAGAT
 AGCTGCTGTACAGTTTACTTTATGATCAGCGCACGGAGTTCAGTTTCACTGACTATAGCACCA
 AAGAGAATGTCCTAGCTGTATCAGAAACATCCGCTATATGATGGTGGAAACAGCTACTGGT
 GATGCCATTTCTTCTCACTGTTAGAAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAGAA
 CTTCTAGTAATTTGTACAGATGGGCAGTCTCATGATGATGTCCAAGGCCCTGCAGCTGCTG
 CACATGATGCAGGAATCACTACTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
 AAAGATATGGCTTTAAACCGAAGAGTCTCACGCTTTTCTTCAACAAGAGTTCACAGGATT
 AGAACCAATTGTTTTCTGATGTCATCAGAGGCATTGTAGAGATTTCTTAGAATCCAGCAAT
AATGGTAACATTTTGACAACATAAAGAAAAAGTACAAGGGGATCCAGTGTGTAAATTTGATT
 CTCAATAATCTGAAATGCTTTAGCATACTAGAATCAGATACAAAACATTAAAGTATGTCAAC
 AGCCATTTAGGCAATAAGCACTCCTTTAAAGCCGCTGCCTTCTGGTTACAATTTACAGTGT
 ACTTTGTTAAAAACACTGCTGAGGCTTCATAATCATGGCTCTTAGAACTCAGGAAAGAGGA
 GATAATGTGGATTAAAAACCTTAAGAGTTCTAACCATGCCCTACTAAATGTACAGATATGCAAA
 TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTTRGLDIRKEKADVLCPPGGCPLEEFVSY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFALKEVGFRRGNSNTGKAL
KHTAQKFFTVDAQVRKGIPKVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCHEQMMCSKTCYNSVNI AFLI
DGSSSVGDSNFRMLLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTEFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCGCCACCGCGCCGCTCCCGCATCTGCACCCGAGCCCC
GGCGGCTCTCCCGGGGAGCGAGCAGATCCAGTCCGGGCCCGAGCGCAACTCGGTCCAGTCG
GGCGGCGGCTGGGGCGCAGAGCGGAGATGAGCAGCGGCTTGGGGCCACCTGCTGTGCTGCTG
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCGCGGCTCTCAGCTACCCGAGGAGGAGGCCACCTCAATGAGATGTTCCGCGA
GGTTGAGGAAGTGTATGGAGGACACGAGCACAAATTGCGCAGCGCGGTGGAAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTTGGCAAACTTACCTCCCAGCTAT
CACAAATGAGACCAACACAGACACGAAGGTTGGAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACACGAGCTGGACAAATGGTCTTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCCCAGC
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGTGTCTGGGGTCACTGCACCAAAA
TGGCCACCAGGGGCGAGCAATGGGACCATCTGTGACAAACAGAGGGACTGCCAGCCGGGGCTG
TGCTGTGCCCTTCCAGAGAGGCTGTGTTCCCTGTGTGCACACCCCTGCCCGTGGAGGGCGA
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCAGTGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGGAGCCGTGACCAAGATGGGGAGATCCTGTGCTGCC
CAGAGAGGTCCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGGAGCTGCGGCTGCCGCCGCT
GCAGTGTCTGGGAGGGGAAGAGATTAGACTCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTATTTCCCCAGGTGTGTGCTTTAGGCGTGGGCTGACCAGGCTTCTCTCTACA
TCTTCTTCCCGATAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTTGTTTCAGC
TCCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGCTGCTTTGCCTCTACCAGTTGGCAG
ACAGCCGTTTGTTCATCATGGCTTTGATAATTGTTTGAGGGGAGGAGATGGAAACAATGTGG
AGTCTCCTCTGATTTGGTTTTGGGAAATGTGGAGAAGAGTGCCCTGCTTTGCAAAACATCAA
CCTGGCAAAAATGTCAACAAATGAATTTTCCACGCACTTCTTCCATGGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTTCATCC
AGCAGTGTTGCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATTC
CCTCTCTCAGCACAGCCTGGGGAGGGGGTCAATTGTTCTCCTGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCACACAGCTAGTGAAGACCAAGAGCAGTTTCAT
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCACACCAGCCTTGGTGCCACCAA
AAGTGCTCCCCAAAGGAAGGAGAAATGGGATTTTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAACTAATTTCTACATCCCTCTAAAAGTAAACTACTGTTAGGAACAGCAGTGTTCTTCAC
AGTGTGGGCGACCGCTCCTTCTAA7GAAGACAATGATGATTGACATGTCCTCTTTGGCAGT
TGCATTAGTAACTTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACTTGCAAGAAACA
GTACTTAGGTAAATTGTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC
TGAAGAACAATTATCAACACGCTGGAGAAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTTCAGGTTGCTCA
TGGACTGTTGCCACCATGTATTCATCCAGAGTTCCTAAAGTTTAAAGTTTACAGATGATTGTA
TAAGCATGCTTCTTTTGAGTTTAAATTTAAATATAAGATAAAGATAGGTTGCATTGACAAATCAAGC
ATAAATCACTTCAACTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYQEEATLNEMFREVEELMEDTQ
HKLRS AVEEMEAEAAAAKASSEVNLANLP SYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGRMLCTRDSECCG
DQLCVWGHCTKMATRGSGNTICDNQRDCQ PGLCCAFQ RGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCP CASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELDLERSLTEEMALGEPAAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTAAAGAGTTAGAGAACCTACCTCACAATCTCTCTGGGCTCAGAAGGACTCTG
 AAGATAACAAATAATTTTCAGCCCATCACTCTCTCTCCCTCCCAACACACATGTGCAATGTACACACACACATACA
 CACACATACACCTTCTCTCTCTCTCACTGAAGACTCAGTCACTCACTCTGTGAGCAGGTCTATAGAAAAGGACAC
 TAAAGCCTTTAAGGACAGGCTGGCCATTACCTCTGCAGCTCTTTTGGCTTGTGTAGCTCAAAAACATGGGAGGGG
 CAGGGCACGGTGACTCACAACCTGTAAATCCAGCATTTTGGGAGACCGAGGTGAGCAGATCACTTGAAGTTCAGGAG
 TTCGAGACAGGCTGGCCAAATGGAGAAACCCCATCTCTACTAAAAATACAAAATTTAGCCAGGAGTGGTGGC
 AGGTGCTCTGAATCCAGCTACTCAGGTGGCTGAGCCAGGAGAATCGCTTGAATCCAGGAGCGGAGGATGCAGT
 CAGCTGAGTGACCGCTGCACTCCAGCCTGGGTGACAGATGAGACTGTGTCTCAAAACAAACAAACCGGAGGA
 GGGGTAGATAGTCTCTCTGCAACCTCTTAACTCTGCATCTCTCTTCCAGGGCTGCCCTGTATGCGGCCCTG
 CCAATGACTGAGCAGGCGCCAGCCCGAGGAGCAAGGAAGAGAAGGCATATTGAGGAGGCGCAAGATGACGCGCCG
 GTGTAGAATGACTGCCCTGGGAGGTGTCTCTTGGGCCCTGGCAGGGTTGCTGACCCTTTACCTCTGCAAAACACA
 AAGAGCAGGACTCCAGACTCTCTTGTGAATGTGTCCTGCCCTGCAGCTCCACCATGAGGGCTTCTCGTGGCCCC
 ACTCTTGTGCTAGCTTGGGTGGCTGCTGGCCACTGCCACTGTGCCGTGGTACCTGGCATGTTCCCTGCCCCCCCTCA
 GTGTGCTGCCAGATCCGGGCCCTGGTATACGCCCCGCTCGTCTACCGCGAGGCTACCACTGTGGAATGCAATGA
 CCTATTCTGACCGGCACTCCCCCGGCACTCCCGCAGGCACACAGACCTGTCTCTGCAAGGCAACAGCATTGT
 CCGTGTGACCAAGATGAGCTGGGCTACCTGGCCAACTCACAAGAGCTGGACCTGTGCCGAGCAACGCTTTTCGGA
 TGCCCCGAGCTGTGATTTGAGTGCCTGCCAGCTGCTGAGCCTGCACTAGAGGAGAACAGCTGACCGCGCT
 CCGGAGCCACAGCTTTTGACGGGCTGGCCAGCCTACAGGAACCTCTATCTCAACCAACACAGCTCTACCCGATCGC
 CCGCAGGCGCTTTCTGGCTCTCAGCACTGTCTGCGCTGCACTCAACTCTGTCGAGGCACTGAGGCGCAATGAG
 CAGCTGGTTTGAATGTGCTGCCAACTTGGAGATACATCATGATTGGCGGCAACAGGTAGATGCCATCTCGGACAT
 GGCTCTCGGCCCTTGGCCAACTCCGTAGCCTGGTGTAGCAGGATGAACCTTGGCGGAGATCTCCGATCATGTC
 CTGGAGGGGCTGCAAAAGCTGGAGAGCCTCTCTCTATGACAACAGCTGGCCCGGGTGGCCAGGCGGGCACT
 GGAACAGCTTCCCGGCTCAAGTTCTTAGACTCAACAGAACCCCTCCAGCGGTAGGCGCGGGGACTTTTGC
 CAACTGCTGTCACCTTTAAGAGCTGGGACTGAACAACTGAGGAGCTGGTCTCCATCGACAACTTTGCCCTGGT
 GAACTCTCCCGAGCTGACCAAGCTGGACATCAACAAATAACCAACCGCTGTCTTCCACACCCCGCGCTTCCA
 CCACCTGCCCGAGATGAGAGCTCATGCTCAACAAACACGCTCTCAGTGGCTTGGACACAGCAGACGGTGGAGTC
 CCTGCCCAACCTGTCCGAGTACTCTCCAGGCAACCCCATCCGCTGTGACTGTGTCTCATCCGCTGGGCCAATGC
 CACGGGCAACCGGTGACCGCTTCACTGAGCCGCAATCCACCTGTGTGCGGAGCTCCGGACCTCCAGCGCTCCC
 GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACATGTGTGCCCCATCTCCCCACAGAGCTCCCCCGAG
 CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCTGCTCCGGGCACTGGCCGAACCCGACCTGCTACTGT
 GGTCACTCCAGCTGGGCTTGCATGACACCTGCCCATGCAAGGAGGTACCGGCTGTACCCGAGGGACCTT
 GGAGCTCGGAGGGGTGACAGCAGAAGAGGCGAGGCTATACACTCTGAGCTGTGTCTGAGCCTGGCAGCTGGGC
 TAAGACGGTTAGTGTGTTGTGGGCCGTCTCTCTCCAGCCAGGCGAGGCAAGAGGACAGGCGGAGCTCCG
 GGTGCAAGGAGACCCACCCCTATCACAATCTGCTATCTTGGGTCAACCCACCAACAGATGTGCCCAACCTCAC
 CTGTTCCAGTGCCTCTCTCTCCGCGGCCAGGGGGCCACAGCTCTGGCCCGCTGCTCTCGGGAAACCCACAGCTA
 CAACAATTAACCGCTCTCTCAGGCCACGGAGTACTGGGCTGCTCTGCAAGTGGCTTTGCTGATCCCAACCCA
 GTTGGCTTGTGTATGGGCCAGGACCAAGAGGCCACTTCTTGGCCACAGAGCTTTAGGGGATCGTCTGGGCTCAT
 TGCCATCTGGCTCTCGCTCTCTCTCTCTGGCAGCTGGGCTAGCGGCCCACTTGGCAGGCGCAACCCAGGAA
 GGGTGTGGTGGGAGGCGGCTCTCCCTCCAGCTGGGCTTCTTGGGCTGGAGTGGCCCTTCTGTCGGGTTGT
 GTCTGCTCCCTCTGCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCTCTAGAAGGGAGACACTGTTGCC
 ACCATTGTCTCAAAATTTCTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTACCAAA
 AGAGAGACAGCTCGGCGGCACTGCCCTGCCAGGAAGGACATGGACCAAGCTTGTGAGGCTCGGAGCTGGGC
 CAAGACAGATGGGGCTTTGTGGCCCTGGGGGTGCTTCTGCAAGCTTGAAAAATTTGCCCTTACCTCTTAGGGTCA
 TCTCTGTGCCAATCTCTAGGAACATCTCCAAGGAACAGGAGGACTTGGCTAGAGCCTCTGCGCTCCCATCTT
 CTCTCTCCAGAGGCTCTTGGGCTTGGCTTGGCTGTCCCTACCTGTGTCCCGGGCTGCACCCCTTCTCTCTC
 TTTCTTCTGTAGCTCTCAGTGTCTTGTCTTGTCTTGTGCTTGTGCGCTTCCAGGAGGCTGAGGAGGCGCATCTC
 CTCGCGGGCTGCCCTCAATGTGGGAGTGACCCAGCCAGATCTGAAGGACATTTGGGAGAGGATGCCAGGAA
 CGCTCATCTCAGCAGCTGGGCTGGGCACTCGAAGCTGACTTTCTATAGGCACTTTGAGGCTTTGTGGAGAA
 ATGTGTCACTCCCCCAACCCGATTCACTCTTTCTCTGTCTTTGTAAAAATAAAATAAATAAACAATAAA
 AAAA

0504055.074304

FIGURE 87

GCAAGCCAAGGCGCTGTTTGAGAAGGTGAAGAAGTTCGCGACCATTGTGGAGGAGGGGGACATTGTGTACCGCCT
CTA**ATG**CGGCGAGACCATCATCAAGGTGATCAAGTTTCATCTCATCATCTGCTACACCGCTTACTTACGTGCACAA
CATCAAGTTTCGACGTGGAGCTGACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCACCC
CCTGGCCACACTCTTTCAAGATTCTGGCGTCTTCTACATCAGCCTAGTCATCTTCTACGGCCCTCATCTGCATGTA
CACACTGTGGTGATGCTACCGCGCTCCCTCAAGAAGTACTCGTTTGAGTGGATCCGCTGAGGAGAGCAGCTACAG
CGACATCCCCGACGCTCAAGAAGCACTTCGCCTTCATGCTGCACCTCATTGACCAATACGACC CGCCTCTACTCCAA
GCGCTTCGCGCTCTCTCTGTGCGGAGGTGAGTGAGAACAAAGCTGCGCAGCTGAACTCAACCAACGAGTGGACGCT
GGACAAGCTTCGGCAGCGCTCACCAAGAACGCGCAGGACAAAGCTGGAGCTGCACTCTGTTTCATGCTCAGTGGCAT
CCCTTGACATCTGTTTGACTGCTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCCCTCATCCGCG
CAGCATTTGCCAGCTCAGCGGCTCAAGGAGCTGTGGCTCTACCAACAGCGGCGAAGATTGAAGCGCCTGGCCT
GGCTTCTGTGCGCAGAACCTGCGGCGCTGCACATCAAGTTTACCGACATCAAGGAGATCCCGCTGTGGATCTA
TAGCTTGAGACACTGAGGAGGCTGCACCTGACGGGCAACCTGAGCGCGGAGAACAAACCGCTACATCGTCATCGA
CGGGCTGCGGGAGCTCAAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGGTGGTCAC
AGATTGGGCGCTGCACCTGCAGAACTGCTCCATCAACAATGAGGGCACCAAGCTCATCTGCTCAACAGCCTCAA
GAAGATGGCGAACCTTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCCACTCCATCTTCAGCCT
CCACAACCTGCAGGAGATTGACCTCAAGGACAAACACTCAAGACCATCGAGGAGATCATCAGCTTCCAGCACCT
GCACCGCTCAGCTGCTTAAAGCTGTGGTACAAACCATCGCCTACATCCCACTGCAGATCGGCAACCTCAAGAACT
CTACCTGGACGCTCTACCTGAACCGCAACAGATCGAGAAAGATCCCCACCGAGCTCTTCTAATGCGCCAGCTCGG
CTACCTGGACCTCAGCCACCAACCACTGACCTTCTCCTCGCGACATCGGCTTCTGACAACTCCAGAACTCCAGAACT
AGCCATCAGCGCCCAACCGGATCGAGAGCTCCCTCCGAGCTCTTCCAGTGC CGGAAGCTGCGGCGCTGCACCT
GGGCAACCACTGCTGTCAGTCACTCCCTCCAGGGTGGGCGAGCTGACCACTGACCGAGATCGAGCTGCGGG
CAACCGGCTGAGGTCTGCTGTTGGAGTGGGCGAGTGCCACTGCTCAAGCGCAGCGCTTGGTGGTGGAGGA
GGACCTGTTCAACACATGCGCACCGGAGTGAAGGAGCGGCTGTGGAGGCTGACCAAGGAGCAGGCT**CG**CGAG
GCGGCGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCGAGGCGGCGAGGCTAGCTTCTCCAG
AACTCCCGACAGCCAGGACAGCTTCGCGGCTGGGCGAGAGCTTGGGCGCGCTTGTGAGTCAGGCGAGGCGAGA
GGACAGTATCTTGGGGCTGGCCCTTTCTCCCTCGAGACTCAGTCCCCCAGGGCAAGTGCTTGTGGAGGAG
AGCAAGTCTCAAGAGCGCATGATTGGATAATCAGGGTCTCTCCCTGGAGGCGAGCTTCCGCCAGGGGCTGAG
CTGCCACAGAGGTTCTGGGACCTCACTTTAGTTCTTGGATTATTTATTTTCTCCATCTCCCACTCTCCCTCATCC
AGATAACTTATACATTTCCCAAGAAAGTTCAAGCCAGATGGAAGGTGTCAGGGAAGGTGGGCTGCTCTTTCCCT
TTGTCTTATTTAGCATGCGCCCGGGCATTAAACACCACTGGACTCAGCAGAGTGGTCCGGGCGAACAG
CCATGGGACGCTACCCAGCAGTGC CGGGCTGGGCTCTGCGGTGCGGTCCAGGGAGAGCAGGCTCCAGCTGGA
AAGGCCAGGCTGGAGCTTGCTCTTCAGTTTTTGTGGCAGTTTAGTTTTTTGTTTTTTTTTTTAAATCAAA
AAACAAATTTTTTTTAAAAAAAAGCTTTGAAAAATGGATGGTTTGGGTATTAAGAAAGAAAAAAAACCTTAAAAAA
AAAAGACACTAACCGGCAGTGGATTGGAGTCTCAGGGCAGGGTGGCAGTTTCCCTTGAGCAAAAGCAGCCAGAGT
TGAACTGTGTTTCTTTCCCTGGGCGCAGGGTGCAAGGTGTCTTCGCGATCTGCTGTGACCTTGGTCCAGGAGTT
CTATTTGTTCTGGGAGGAGGAGGTTTTTTTGTGTTTTTTTGGGTTTTTTTGGTGTCTGTTTTCTTCTCCTCC
ATGTGTTCTGGCAGCACTCATTTCTGTGGCTGTGCGCCAGAGGGAATGTTCTGGAGTGCACCAAGAGGAGGAG
ACTCGGTTGGCTAATCCCCGATGAACGGTGTCTCATTCGCACCTCCCTCTCGTGGCTCCCTGCTCTCCA
CGCACAGTGTAAAGAGCAAGAGGAGCACTTCGCCACAGCTTTGTTTCCCACTCCCTGCGGCATGGTGTGT
CAGTGTGCTCGGATGGGAGGTCGCCCCGAGGAGGCGAGGCTTGGTTCCAAGCCGTTCCCGCTCCCTGGCGC
TAGGCTGACACAGCCAGTGGCAGCTGGCTGGCTGGAAGCCAACTGCTTTAGATCACTCGGTCGCCACTT
AGAAGGCTCCCGCCTTAGATCAATCAGTGGACATGAGGCAGCTTTTAGAGTCTTCTGCTTAATGATATGT
CCATCGCTCTGTGCTGCTCACTTTCTGCGTGTGATGATATACTCAGAAATAATGCACACTAG
CCTCTGAACACATGAAGCAAAATCCGTACATGTGGGTCTGAACCTTGTAGACTCGGTCACAGTATCAAATAAA
ATCTATAACAGAAAAA

0000435-07234

FIGURE 88

MRQTIKVIKFIILICYTVYYVHNKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHLFMLSIGIPDTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFTDIKEIPLWI
YSLKTLLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIETIISFQ
HLHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFCRKLRLHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCA**TG**GAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCTGCCGCTGCTGCTGGGCTGAACGCAGGAGCTGTCAATTGACT
GGCCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGTGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGTGAAACTTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCAACGAAAACCACTGGCTCCAGGCTGCCAGTCTCCATTATT
GTGGATAATCCCGTGGGCACCTGGGTTCACTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCAGACAGTTCATTCTACATTTTCTCAGAGTCTATGGAGGAAAAATGCGAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTCAAGCGAGGACCACCAAGTCAACTTTGCGGGGGT
TGCCTTGGGTGATTCTCGGATCTCCCTGTTGATTGCTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTTCTCGAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTTGAACAGAACACAGATGGGGTGAACCTTATAACATCTTAACTAAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGCCACCTAGTTTGTCTTTGTGAGCGC
CACGTGAGACACCTACAACGAGATGCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAAATATTCTCGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGTGAGGAGGAGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTGAGGAGGCTG
GGTGCGGAACTGAAGTGGCCAGAACTGCCTAAATTCAGTCAGCTGAAGTGAAGGCCCTGT
ACAGTGACCCATAATCTTTGGAAACATCTGCTTTTGTCAAGTCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAGCTGGTCATATGGTTCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGAAGTCAAGAA**TAG**GATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTTGGAATATTATTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLDSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDSVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNGLYRE
ATELWGKAEMII EQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIPEDQSWGQATNVFVNMEEDFMKPVISIVDELLEAGINVTYNGQLDL
IVDTMGQEAWVRKLKWPPELPKFSQLKWKALYSDPKSLETSAFVKS YKNLAFYWILKAGHMVP
SDQGD MALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA
GGGAGCCTGCGCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTACCCCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCTCCAGGAAGTTCAGGTGCGCCATCATAAACA
ACTCTATGTGCAACCACCTCTTCTCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGGCTGTG
GTCGGCCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACCTTTGAGTGGATCCAGAAG
CTGATGGCCCAGAGTGGCATGTCCAGCCAGACCCCTCCTGGCCACTACTCTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCCGGTCTGAGCCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTTCTCTTCTGTCTGTTTGGTAATAAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTTCTTCAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLLALLLARAGLRKPESQEAPLSGPGRRVITSRIVGGEDAELGRWPWQGSRLRW
DSHVCVGSLLSHRWALTAACHFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWSGVCGRPNRPGVYTNISHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

00000000000000000000

CCACACGCGTCCGCGGACGCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTTAGGGCT
CTTTTGCCCTCATCTCTCTGCGCAATGCAGTTAAGCCCGGAGCCGACGACGGGAGGACCG
TGCCCCAGGCTGGGTGTCCCTGGCGCGTGCAGACCTTGAGGAAGAGCTGAGTCTCACTCTT
GCCCTGAGACAGCAGAAATGTGGAAGAACCTCTCGGAGCTGTGTCAGAGCTGTGTCGGAATCCGAG
CTCTCTCTCAATACGGAAATACCTAGACCTTAGAAGATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCTCCACACGGTGCAAAATATGCTCTTTGGCAGCCGGAGCCCAAGATGGCAATTCT
GTGATCACACAGGACCTTTCTGACTTGTCTGCTGAGCATCCGACAAGCAGAGCTGCTGCTCC
TGGGGCTGAGTTTTCATCACTATGTGGGAGGACCTACGAAACCCTATTGTTGAAGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCCTTGGGCCCCCATGTGGACTTTGTGGGGGGACTGCACCG
TTTCCCCCAAGTATCTCCCTGAGCGCAACTCTCTGAGCCGAGGTGACAGGGAATGTAGGCCCT
GCATCTGGGGGTAAACCCCTCTGTGATCCGTAGCGATACAACCTTGACCTCAAGAAGCTGG
GCTCTGGCACCGACAATAACAGCCAAAGCTGTGTCGCCAGTTCTCTGGAGCAGTATTTCCATGAC
TCAGACCTGGCTCAGTTTACGTGCGCTCTCTCGTGGCAACTTTGCACATCAGGCATCAGTAGC
CCGTGTGTTGGACAACAGGCCGCGGGCCGGGATCGGGATTGAGCCAGCTAGATGTGAGT
ACCTGATAGTGTCTGTGTCACCAATCTCCACCTGGGTCTACAGTAGCCCTTGGCCGCGATGAG
GGACAGGAGCCCTTCTCTGAGGTGCTCATGCTGCTCAGTAATGAGTACGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCGCTCGGGTCTACCTCTGCTCTTGCCTCAGGTGACAGT
GGGGCCGGGTGTGTTGCTGTCTCTGGAAGACACCAAGTTCGCGCCCTACCTTCCCTGCTCCAG
CCCCTATGTCATACAGTGGGAGGCAATCTCTCCAGGAACCTTTCTCATCACAAAATGAAA
TTGTTGACTACTACAGTGGTGGTGGCTTCCAGAAATGTGTTCCCAAGCCGCTTATCCATCAGGAG
GAAGCTGTAAACGAAGTTCTGAGCTATAGCCCCACCTGCAACCATCAGTTACTTCAATGC
CAGTGGCCGCTGCCATCCAGATGTGGCTGCATCTTCTGATGCTCATGGTGGTGCAGCAACA
GAGTGGCCATTCATAGGTTGTCGGAACCTCGGCTCTACTCAGTGTGTTGGGGGGATCTCTA
TCTTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTTGGCTTTTCTCAACCCAG
GCTCTACAGCAGCATGGGGCAGGTCTTTTGATGAACCGTGGCTGCATGAGTCTGTGCT
TGATTAAGAGAGTGAGGGCCAGGTTTGTCTGTGCTGTGCTGGGTGGATCTGTGAACAGGC
TGGGGAGACCAACCTTCCAGCTTTGCTGAAGACTTACTCAACCCCTGAGCCCTTCTCAT
AGGAGAGATGGCTTGTCCCCTGCCCTGAAGCTGGCAGTTCAGTCCCTTATCTGCCCTGTG
GAAGCCCTGCTGAACCTCAACTATTGACTGTCTGCAGACAGCTTATCTCCCTAACCCTGAAA
TGCTGTGAGCTGACTGACTGCCAACCCATCATGCTCCATATACTCAGGTCTCCCTTACT
CTTGCTTGAATTTCTCAATAAGATGTCTGAACTAGCAATTTTTGATGCTCTCTCCCTCCG
ATCTCATCTTTCTTTTCAATCAGGCTTTTCAAAGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCAATCCCAATCTACGCAAGGAGACCTTACTGTCACTGTTTACTCT
TTCTACCTGCATCTCAGAAACAATGGCTCAGTGATACCTTCAATCTTTGCTTTATG
GCCTTTCATCATAGTTGTCCCACTCCCTCTCTTACTTACTGCTCCAGGTCTTAACTTCTGT
ACTACTCTGTGCTTCTCTCTCATCAATTTCTGCTTCTTCAATGGAATGCTGACCTTCATG
TCCATTTGTAGATTTTGTCTCTTCTCAGTTTACTTATGTGCCCTGGAACAAATCACTGACA
TCAACAACCATTACCATCTCTACTAAATAGACTTTCTATCCAATAATGATTGATACCTCAA
TGTAATAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQQCHSVITQDFLTCWL
SIRQAELLPLPGAEFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLF
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAAAGLTLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPVWSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPWDFVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCTCCCGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC
GGGCTGCTCGGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCCTTCTC
TTCTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTCCCCCTGGAAACCACTTG
GCTTGATACCGCTCCCTGTGCTTGGCCCCAGTCTACCTCAATTTAGCCAAGCCAGACT
TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTATGTGGACCCAGTGTCTATAAGGGAACT
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC
AGGTTTACGATTTTTTGGGAAGGACTTCCTGCTCAACTACCTTTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCTTGGTGGCAGAGAAGCATGTCCTCACAGTGGCCCACTGCA
TACACGATGGA AAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCCTAAAGCCC
AAGTTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCCGAGCAGATGAA
ATTTAGTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACCTCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACTTCTC
TGGTTATGACAATGACCGACCAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGTCTTACCAGCAATGCGATGCCCAGCCAGGGGCCAGCGGGTCTGGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTTCAGG
GCACCAAGTGGGTGGACATGAATGGTTCCCCACAGGATTTCAACGTGGCTGTCAGAATCACTC
CTCTCAAATATGCCCAGATTTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTTCCTCCTGGCAGCAATTAAGGGTCTTCATGTTCTTATTTTAGGAGAGGCC
AAATTGTTTTTTGTTCATTGGCGTGACACGTGTGTGTGTGTGTGTGTGTGTGTGTGAAGGTG
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAACCTG
GTTTGTGTATCATATCATATATCATTTAAGCAGTTTGAAGGCATACTTTTGCATAGAAATAA
AAAAATACTGATTTGGGGCAATGAGGAATATTGACAATTAAGTTAATCTTCACGTTTTTGT
CAAACTTTGATTTTTTATTTTCATCTGAACCTGTTTCAAAGATTTATATTAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

FIGURE 96

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIYILSSSGDGAQHRDSSSGKS
RRKRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKL RVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDVKDETYDLLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNAVVRITPLKYAQICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGCCATGGTGTTT
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTGTGGGCGGCGAGACAGCACTGACAGCGAGTGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCCTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCCACTGTTTTCAAGGACAACCTGAACAAACCATACCTGTTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAACCTGGCTCTCGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCCTGTGTATTCTTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCGTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCTTGC
CCCACCCTCAGACCCTGCAGAAGCTGAAGGTTCCCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCTCGGGCGGTTTCCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGCCCCGGACGGCTGCTGCGGAAAGGAAACCCCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGGCCCAACGGCCTCATGTCCCCGCCCCAC
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTTGTGTATATAAATGTTAATGATTTTAT
AGGTATTTGTAACCTGCCACATATCTTATTTATTCCTCAATTTCAATAAATATTATTAT
CTCCAAAAA

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTTCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCTTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGGCCAC
AAACAAGGAGCGCGGGCGCCGCGCGGAGAACTGTTCGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGTTGTTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCTTACCTGGTAACTGAGGCCCCATCCTTCCGGGCGACTGA
AGCATCAGACTCTAGGAAAAATGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACCTTCCCTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAAC
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCCCAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCAGAGAACTCTTGGAACCCAAGATGTCCCTGACAGGGGCAAG
GGAACTCCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG
AGGTCTTGGCCTCAGTTTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTTGTGTGAGGCTGAACCTCGGGCCCTGGTCACTGTGTGGGGCCCTCTCCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCACCTCAAAGGG
TGAAGAGGTGAGCTGTCTCTCTGTCATCTTCCCCACCCTGTCCCCAGCCCCATAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCCCTCCCTCCTGAGTCCTGGGGTGGGAGGATTGTAGGGAGCT
CACTGCCTACCTGGCCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTTCTAGGGGAGATGAAGGACAAGCCCCCATGGAGTGGGGTTCT
TTTGAGTGGGGGAGGCAGGACGAGGGAAGGAAAGTAACCTCTGACTCTCCAATAAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLLPLLLLLLVATTGFPVGALTDEEKRLMVELHNLRYAQVSPITASDMLHMRWDEE
LAAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLGVEETNIELLVVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSFRAATEASDSRKMGTSPSSLATGIPAFVLVTEV
SGSLATKALPAVETQAPTSLATKDPSPMATEAPPVTEVPISILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSSLPGAEGDPKPSVV
SGLNSGFGHVWGPLLGLLLLPLVLGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAAC TGAAGTCAGGCTTTTCATTGGGAAGCCCCCTCAACAGAATTCGGTCATTCTCCAAGTATATGGTGGAGCT
 ACTTCGTGTGTTCTCCCTCTGCTGTGCTTTTTCACATTAGCAGACCGGACTTAAGTCAACACAGATTATCTTCATCA
 CAGGCGAAGTTCATGAGCCACTCTCAAAGCCTTCGAGAAGTGAACCTGAACCAACATGAATTTGGAGACCAATCC
 AAATCTGGGAGCCAGCTCTCGGCAAAATATTACACTTCTCTCCTTGGCTGGAAACAGGATTTGTGAAATACTCCCTGA
 ACATCTGAAGAGTGTTCAGTCTCTGTAACCTTTGGACCTTAGCAGCAACAATATTTTCAGAGCTCCAAACTCGATT
 TCCAGCCCTCAGCTCAAAATATCTGTATCTCAACAGCAACCGAGTCACTCAATGGGAACCTGGGTATTTTGACAA
 TTTGGCCCAACACACTCTGTGTGTTAAAGCTGAACAGGAACGAATCTCAGACTTCCCAACCAGATGTTTTTAAACT
 GCCCACAATCTGCAACATCTCGAATTTGAACCGAAACAGATTTAAAATGTAGATGGAGCTGACATCTTCCAGGGCTTTGG
 TGCTCTCAAGTCTCTGAAAATGCAAAAGTGAATGCAAGAACTTATGGATGGAGCTTTTGGGGGCTGAGCAAC
 CATGGAAATTTTTCAGCTGGACCAATAACAACTTAACAGAGATTACCAAGGCTGGGCTTTACGGCTTCTGTATGCT
 CGAGCAACTTCACTTCAGCCAAATGCCATCAACAGGATCAGCCTGTATCGCTGGAGTCTCTGCCAGAAGCTCAG
 TGAGCTGGACCTTAATCTTCAATCACTTATCAAGGTTAGATGATTAAGGCTTCTTGGCCTTAAGCTTACTATAATAC
 ACTGCACATTTGGGAACAACAGAGCTCAGCTACATTTGCTGATTTGTGCCCTTCCGGGGCTTTCCAGTTTAAAGACTTT
 GGAATCTGAAGAACAAATGAAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTCGGGCTTGACAAATGAG
 CGACTGATATCTCCAAGGAAATCGGATCGGTCTATTACTAAAAAGCCTTCACTGGTTTGGATGCATTTGGAGCA
 TCTAGACCTGAGTGACAAACGCAATCATGTCTTTACAGGCAATGCATTTTTCACAAATGAAGAACTGCACAAAT
 GCATTTAAATACATCAAGCCTTTTGTGCGATTGCCAGCTAAATGGCTCCCAGCTGGGTGGCGGAAACCAACTTT
 TCAAGACTTTTGAATCGAGTTTGTGCCATCTTCAGCTGCTAAAAGGAAGAGCAATTTTGTCTGTAGCCAGATA
 TGGCTTTGTGTGTGATGATTTTCCCAAACCCAGATCACGGTTTCAGCGAGAACACAGTCCGCAATAAAAGGTTT
 CAATTTGAGTTTCATCTGCTCAGCTGCCAGCAGCAGTGTATCCCAATGACTTTTGTGCTGGAAAAAGCAATGA
 ACTACTGTCATGATGCTGAAATGGAAAAATATGCAACCTCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACCA
 CATCTTTCGGCTGCGGAGGTGGAATTTGCCAGTGAGGGGAAATATCAGTGTGTCATCTCCAACTCTTTGGTTT
 ATCTCTACTCTGTCAAAGCCAAAGCTTACAGTAATAATGCTTCCCTCATTCACCAAGACCCCATTTGATCTCACCAT
 CCGAGCTGGGGCCATGGCCAGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCAGATAGCCTGGCAGAAAGGA
 TGGGGGCACAGACTTCCAGCTGCACGGGAGAGACGATGCATGTGATGCCCGGAGGATGACGTGTTCTTTATGCT
 GGAATGGAAGATAGAGGACATGGGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTTCAGCAATGC
 AACTCTGACTGTCTAGAAACACCATCATTTTTCGGGCCACTGTTGGACCGAACTGTAAACCAAGGGAGAAACAGC
 CGTCTACAGTGCATTTGCTGGAGGAAGCCCTCCCCCTTAAACTGAACTGGACCAAGAGTGAATAGCCCATTTGTGCT
 AACCGAGAGGCACTTTTTCAGCAGGCAATCAGCTTCTGATTATTTGTGGACTCAGATGTCAAGTGTGCTGGGAA
 ATACACATGTGAGATGTCTAACACCTTGGCACTGAGAGAGGAAACGTGCGCTCAGTGTGATCCCACTCCAAC
 CTGCGACTCCCTCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTGCTGATCATAG
 CGTGGTTTGTGCTGTGGTGGGCAGCTCACTCGTGTGGTGGTGCATATATACCAACAAGGCGGAGGAATGAAGA
 TTGCAGCATTACCAACAGATGAGACCACTTGCCAGCAGATATTCCTAGTTATTTGTCACTCTCGAGGAAAGCTT
 AGCTGACAGGAGGATGGGTACGTGCTTCAGAAAGTGAAGGCCACCACTGTTGTCACTCTTCAGGTCTCGG
 ATTTTCTTCCACCAATGACAGTAGTGGGACCTGCCATATTGACAAATAGCAGTGAAGCTGATGTGGAAGCTGC
 CACAGATCTGTTCTTTGTCCGTTTTCGGGATCCACAGGCCCTATGTAATTTGAAGGGAAATGTGTATGGCTCAGA
 TCCTTTTGAAACATATCATACAGGTGTCAGTCTGACCCAGAAACAGTTTAAATGGACCACTATGAGCCAGTGA
 CATAAAGAAAAAGGAGTGCTACCGATGTTCTCATCTTCAAGAGAATCTGCGAACCGGAGCTTCAGTAATATATC
 GTGGCCCTCACAATGTAGGAGAGCTACTTAACTAGTTACTCTCAATGAAGGACCTTGAATGAAAAATCTGTG
 TCTAAACAAGTCTCTTTAGATTTTAGTGCAAAATCCAGAGCCAGCGTCGGTTGCCCTCGAGTAATCTTTTCATGGG
 TACCTTTGAAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTTCAAGCTTTGGACAGCCATCAGATTTGTCAGCC
 AAGAGCCTTTGATTTGAAAGCTCATCTTCCACAGACTTGGACTCTGGGTTCAGAGGAAGATGGGAAATGAAGGAC
 AGATTTTCAGGAAGAAATCACAATTTGTACCTTTAAACAGACTTTAGAAAACTACAGGACTCCAAATTTTCAGTC
 TTATGACTCTGGACATAGACTGAATGAGACCAAGGAAAAAGCTTAACTACTACTCTCAGTCAAGTGAACCTTTTATTTA
 AAAGAGAGAGATCTTATGTTTTCATTTAAATGGAGTTATGAATTTTAAAGGATAAAAATGCTTTATTTATACAGAT
 GAACCCAAATACAAAAAGTTATGAAAAATTTTATACTGGGAATGATGCTCATATAGAAATACCTTTTAAACTA
 TTTTAACTCTTGTGTTATGCAAAAAAGTATCTTACGTAATTAATGATATAAATCATGATATTTTATGTAATTT
 TATAATGCCAGATTTCTTTTATGGAAAAAGTGTACTAAAGCAATTTAAATAAATACCTGCTCTGTACCAATTTT
 TTAATAAGAGTTACTTCAATATATTTTGCACATATATTTTAAATAAATGTGTCAATTTGAA

500145-01301

FIGURE 102

MVDVLLLFSLCLLPHISRDPDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAPFALQLKYLNLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRI SAIPPMMFKLPQLQHLELNRRNKIKNV DGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMEILQLDHNMLTEITKGWLYGLLMLQBELHLSQNAINRISPDAWE
FCQKLESELDTFNHLSRLDDSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSLKTLDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSI TKKAFTGLDALEHLDSLDAIMSLQGNAFSQ
MKKLQQLHLNLTSSLLCDCQLKWLPPQWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAHLRAGG
GEVMEYTTILRLREVEFASGEKYQCVISNHFSSSYSVKAKLTVNMLPSFTKTPMDLTIIRAGA
MARLECAAVGHAPQIAWQKDGDTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTLVLETPSFRLPLLDRTVTKGETA VLQCIAGGSPPPKLNWTKDDSPLVVTER
HFFAAGNQLLIIVDSDVSDAGKYTCMSNTLGTGERGNVRLSVIPTPTCDSPQMTAPSLDDDG
WATVGVVIIAVVCCVVGTSLVVWVVIYHTRRRNEDCSI TNTDETNLPA DIPSYLSSQGTLAD
RQDGVVSSSESGSHHQFVTS SGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCFFLGSTGP
MYLKGNVYSGDPFETTYHTGCSDPDRTVLMDHYEPSYIKKKECYPCSHPSSESCERSFSFNISW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSSLDFSANPEPASVASSNSFMGTFFGKALRRPHLDA
YSSFQFSDCQPRAFVILKAHSSPDLDSSGSEEDGKERTDFQEEHNHICTFKQTLNRYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAAITGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTTGGGTGCCTTGCAAAAAATG
AAGGATGACAGGACCGCAGCTTTCTCTCGAACCAGACGCAATGGATAAACTGATTGTGTCAGAGAGAGAAGGAGAAC
GAAGCTTTTTCTTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAGAAATGAAA
TAAACAGAGTTAGACCCCGCGGGGTTGGTGTCTTGACATAAAATAAATATCTTAAAGCAGCTGTTCCCTCTCC
CCACCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCAAAAAGAAAAAGTATGTTTCATTTTCTC
TATAAAGGAGAAAGTGAAGCCAGGAGATATTTTGGAAATGAAAGTTTGGGGCTTTTGTAGTAAAGTAAAGAACT
GGTGTGGTGTGTTTCTCTTTCTTTTGAATTTCCACAAGAGGAGAGGAAATTAATAATACATCTGCAAGGAAA
TTTCAGAGAGAAAAGTTGACCGCGGACAGTTGAGGCATTGATTGGGGGAGAGAAACAGCAGAGCAGCAGTTGGA
TTTGTGCTTATGTTGACTAAAATTGACGGATAATTGACGTTGGATTTTCTTCATCAACCTCTCTTTTAAAT
TTTTATTCTCTTTGGTATCAAGATCATGCGTTTTCTCTGTTCTTAACACCTGGATTCCATCTGGATGTTGCT
GTGATCAGTCTGAATACTAACTGTTTGAATTCAGAAGGACCAACCCAGATAAATTATGATGTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGTCCTAGGTTTAAACAGGGCCCTATTGACCCCTGCTTGTGGTGT
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGCGGGCTCAGACCTGCCCTTCTGTGTGCTCCTGCAGCAA
CCAGTTGACGAGGTGATTGTGTTCCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACCACACACAGGCT
GCTGAACCTCCATGAGAACCAAAATCCAGATCATCAAAGTGAACAGCTTCAAGCACTTGAGGCACCTTGGAAATCTCT
ACAGTTGAGTAGGAACCATATCAGAACCATGAAATTGGGGCTTTCAATGCTCTGGCGAACCTCAACACTCTGGA
ACTCTTTGACAACTCGTCTTACTACCATCCGAATGGAGCTTTGTATACCTGTCTAAACTGAAGAGCTCTGGTT
GCGAAACAACCCCATGAAAGCATCCCTCTTATGCTTTTAAACAGAAATTCCTCTCTTGGCGCGACTAGACTTAGG
GGAATTGAAAAGACTTTTACATCATCTCAGAAGGTGCTTTGAAGGCTCTGCTCAACTTGAAGTATTTGAACCTTGC
CATGTGCAACCTTCGGGAAATCCCTTAACCTCACACCGCTCATAAAACTAGATGAGCTGGATCTTTCTGGGAATCA
TTTATCTGCCATCAGGCTCGGCTCTTTCCAGGCTTTGATGCACTTCAAAAACCTGTGGATGATACAGCTCCAGAT
TCAAGTGATTGAACGGAATGCCCTTTGACAACCTTCAGTCACTAGTGGAGTCAACCTGGCACAATAATCTTAAC
ATTACTGCTCATGACCTCTTCACTCCCTTGATCATCTAGAGCGGATACATTTACATCACACCCCTTGGAACTG
TAACTGTACACTACTGCTCAGCTGGTGGATAAAAAGACATGGCCCTCGAACACAGCTTTGTTGTGGCCCGTG
TAAACATCTCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACAGAAATTACTTTACATGCTATGCTCCGGT
GATTGTGGAGCCCTCGCAGACCTCAATGTCACTGAAGGACATGGCAGCTGAGCTGAAATGTGCGGCCCTCCACATC
CCTGACATCTGATCTTGGATTACTCCAAATGGAACAGTTCATGACACATGGGGCGTACAAGTGGCGATAGCTGT
GCTCAGTGATGGTACGTTAAATTTCACAAATGTAACGTGTGCAAGATACAGGCATGTACACATGTATGGTGAGTAA
TTCGTTGGGAAATACTACTGCTTCAGCCACCTGAAATGTTACTGACGCAACCACTACTCCTTTCTTACTTTTC
AACCGTCAACAGTAGAGACTATGGAACCGTCTCAGGATGAGGACCGGACACAGATAACAATGTGGGTCCCACCTCC
AGTGGTCCGACTGGGAGACCAACAAATGTGACCACTCTCTCACACCCACAGAGCACAAGGTCGACAGAGAAAACCTT
CACCATCCCACTGACTGATATAAACAGTGGGATCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
TGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTTCTACAAGATGAGGAAGCAGACCA
TCGGCAAAACCATCACGCCCCCAACAAGGACTGTTGAAATTAATATGTGGATGATGAGATTACGGGAGACACACC
CATGGAAAGCCACTGCCATGCTGCTATCGAGCATGAGCACCTAAATCATATAACTCATACAAATCTCCCTT
CAACCACACAACAGTTAAACAAATAAATTCATAACAGATTCAAGTGACGACCGTTATGTATCCGAATGAA
CTTAAGACAAATGTAAGAGAGACTCAAACTCTAAACATTTACAGAGTACAAAAACAAACATCAAAAAAA
GACGATTTTAAAAATGACACAAATGATGGCTAAATCTACTGTTTCAAAAAGTGTCTTTACAAAAAAACAA
AAAAGAAAAAGAAATTTATTATTAATAAATTTCTATTGTGATCTAAAGCAGACAAAAA

FIGURE 104

MLNKM T LHPQQIMIGPRFNRALFDPLLVL LALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGI STNTRLNLNHNQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNR LTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLAMCNLREIPNLTP LIKLDELDSLGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRAS TSLTSVSWITPNGTVMTHGAYKVRIAVLSDGT LNFTNVTVQDTGMYTCMVNSVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTDNNVGP TPVVDWETTNTVTSLTPO
STRSTEKTFTIPVTDINSIGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
HHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHNTTVNTINSIHS
VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

Refugees

TGGCGGACGCTGCTGCAGCTTGAACCTGTGTCGAGTTGGGCACTCTTTTCGTTTCCCTCTGCTGTTTGGGGGCA
 TGAAGGCGTCTCCGCCCGGGATGAAAGAGCAAGTTGACGGGCAAGCGGAGGAGGAGCGGCACGCGACCGC
 GAGGCGGGCGCTGCACCTTCGCTGGAAGTTGTCGCGGGCCGAGCGCGCGCGTGGAGCTCTGGGTAGA
 GACTACCGCTGACACCGGATGCGAGCGCGCCGAGCTTCGTCGCGCGCGCGGGGTGGGGCTCTGCTGTGCG
 CGGCTCTGGGGCGCGTCTGCGCGTGCAGACGGCGGCTGCGGGGAATCTGGGCGACCCCTCTGGGTGATGCGCC
 GAGCCGCGATGCGCCATCTCTGCGCTGCTCGCTCGGGAGCTCTGTGACATCGACTCTGAAGCGGATCGAGCGCTCT
 CCGAGCGCACTCCGCTCTGGGTGCTGCTGCGCTGGACTTAAGTCAACAAGATTATCTTTCTCAAGGCAAGCTCC
 ATGACGGCACTCTCAAGGCTCTCGAGAGGTGAATCGAAGACAAAGTAATGGAGACCACTTCAAACTCTGGGACCA
 CTCGCGGGAAATATACCTCTCTCTCTGCTGGTGAACAAGGATTTGTGAATACCTCCCTGAACATCTGAAGAAT
 TTTGACGCTCTTGAACCTTTGGACCTTTAGCAGCAACAATATTTTCAGAGCTCCAAATCTGACATTTTCAGCCCTACAG
 CTCAAATATCTGATCTCAACGAGCAACCGAGTACATCAATGAACCTGGGTATTTTGTCAATTTTGGCCAAACACA
 CTCCTCTGTTTAAAGCTGAACGAGAACCGAATCTCAGTATCTCCACCAGATGTTTAAATCGGCCCACTGCAAA
 ACTTCTCGAATGTAAGCAAGAAAGATTAATAATGTATGATGACATGACATCTCAGGCCCTTGGTGCTCTGAAGTCT
 CTGAAATGTCAAGAAGAAATGGATGATACGAAATCTTATGGATGGAGCTTTTGGGGCGTAGCAACATCGAAATTTTG
 CAGCTGGACATCAACACCTACAAGAGATACCAAGAGCTGGCTTTTACGCGTCTGATGCTGTCAGGAATCTTAC
 CTCAGCCAAAGCGCATCAACAGAGTACGCCCTGATGCTGGAGGATTTGCGCAAGAACTCAGTGAAGCTGACCTA
 ACTTTCAATCACTATCTCAAGGTTAGATGATCTCAAGCTCTTGGGCTTAAGCTTAATAATACATGCAATCTGGG
 AACCAACAGAGTCAGCTACATCTTGCTGATTTGGCTCTCGGGGGCTTTCCAGTTTAAAGACTTTTGGATCTGAAGAAC
 ATATGAATTTTCTGGACTATGAAGACATGAATGGTGTTTCTCTGGCTGCACAACTGAGGCGCACTGATACCT
 CAAAGAAATCGGATCGCTCTTATTAATAAAAGCTCTCACTGGTTTGGATGATCTGGAGCATCTAGACCTGAGT
 CAGGACCAATCATGTCTTACAAGGCAATGCAATTTTCACAATGAAGAACTGCAAACTGCAATTTTAATAACA
 TAAAGCTTTTGGCGATTGGCGACTTAAATAGCTTCCACAGTGGGTGGCGGAAACCAATTTGACGCTTTGTA
 CAGGTCAGTTGGTCCCATCTTCAGCTCTAAAGGAAGAAGCATTTTGGCTGTAGCCCAAGCTCTGAGCTTTGTGT
 GATGATTTTCCCAACCCGAGATCACGGTTTCAGCCAGAACACAGATCGCAATAAAGSTTTCAAATTTGAGTTTC
 ATATGCTCAGCTGCGACAGCAGTATGTCCCAATGACTTTTCTGCTGAAGAAGACGAACTGAACATCTGATGATG
 CTGAAATGTGAAATATATGACACTCTCGGCGCCAGCTGGCGAGCTGATGGATATACCAACTCTCTCGGCTC
 CGCGAGGTGGAATTTGCGATGAGGGGAAATCTCAGTGTCTCATCTCCAACTCTGCTTCTCATCTCTCTCTGTC
 AAGGCAAGCTCTACAGTAATATGCTTGGCTCAATTCACCAAGACCCCATGATCTTCCGCTCAGCTCTGTCG
 ATGCGACGCTTGGAGTGTCTGCTTGGCCACACCGACCCCGACATGCTCTGAGGATGGGGGACACAGCT
 TCCGAGCTGCACGGGAGAGCAGATCATGTGATGTCGGAGGATGACGTCTGCGAGGAGGAGGATGAAGATTCGACGATTAAC
 GAGGACATTTGGGTATACAGCTGCAGCTACGAACAGTCGAGGAGGATTTCTATCTCTGGAATGTGAAGATA
 CTAGAACACCATCATTTTTCGGCCACTGTTGACCCAACTGTAAACCAAGGAGGATAGCCGCTCTCATAGTGC
 ATTTGCTGGAGGAAGGCTTCCCTCAATGAACTGAATCGAGCAAGATGATAGCCATTTGGTGTAAACCGAGAGGCC
 TTTTTCACACAGGCACTCACTCTGATATTTGGGCAAGTCTGACCAAGATGATAGCCATTTGGTGTAAACCGAGAGGCC
 ATTTCTCAACGCTTGGCATCAGATGAGAACGATGCGGCTCAGTGTGATCCGATCAACCTCAACCTTCGACATCCCTT
 CAGATGACAGCCCTCATCTGTAGACGATGGGATGGGCACTGTGGGTGCTGATCATACAGCTGGTGTGCTGT
 GTGTGGGCACTGACCTCTGTGGGTGATCATACACCAAGCGGGAGGATGAAGATTCGACGATTAAC
 AACACAGATGAGACCACTTCCGACGAGCAATCTCTAGTTATTTGTGATCTCAGGGAACCTTAGCTGACAGGCCG
 GAGGGTACAGCTGCTTCAGAAAGTGAAGGCAACCAAGCTTTGTGCATCTTCAGGAGCTTAGCTGACAGGCCG
 CAACATCAGCAGTAGTGGGACTGCAATTTGACCAATAGCAGTGTGATGCTGATGTGGAGAGCTGCCACGATCTGTC
 CTCTTGTCCGTTTGGGATCAGCAGGCCCTATGATTTGAAGGGAAATGTGATGCTCAGATCTGTTTGAACA
 CATCATCAGGTTGCACTCTGCACCGAAGACGTTTATATGGACACATGTAGGCCATACATAAAGAAAGAG
 GATGCTACCGATTTCTCATCTCTCAGAGAATCTCTCGGACAGCGAGCTTCAGATAATATCTGGTGGGCTTCACAT
 GTGAGGAGGCTACTTAACTAGTATCTCAATGAAGGACCTGGATGAAATATCTGTGCTAAACCAAGTCT
 CTCTAGATTTTAGTGTCAATTCAGAGCCAGCTCGGTTGCTCGATTAATCTTCTATGGGTATCTTGGAAAT
 GCTCTCAGGAGACCTCCTACCTAGATGCTTCAAGCTTTGGCAGCCATCAGATGTGAGCCAGAGCCCTTTAT
 TTTGAAGCTCATTTCTCCCGACATCTGCACTTGGGTCAGAGAGAGATGGGAAGAACGACGATTTTCAGGA
 GAAATACCATTTTGACTTTTAAACAGACTTGTGAATACTACAGCACTGGAATTTTTCAGTCTTATGACTTGGAC
 ACAATAGACTGAATGAGACCAAGGAAGGCTTACATACCTCACTCAAGTGAACCTTTTATTTAAAGAGAGGAAAT
 CTATGTTTTTTAAATGGAGTATGAATTTTAAAGAGAGTAAAGTCTTTATTTATACAGATGAACCAAAATAC
 AAAAGATTTAGAAATTTTATATCTGGGAATGATGCTCATATAAGAACTCTTTTAAATATTTTAACTTTG
 TTTTATGCAAAAGAGTATCTTACTGAAATTAATGATATAAATCATGATGATTTTATGATTTTATAATGGCAGA
 TTTCTTTTATGGAAATGATTTATTAAGCAATTTTAATAATACCTGCTGTACCAATTTTAAATAGAAGAT
 ACTTCATATATATTTGCACATATATTTATAAAATGTGTCAATTTGAAAAAAAATAAAAAAAAATAAATAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAERPCPTTCRCGLGDLDDCSR
 KRLARLPEPLPSWVARLDLSDHNRSLFISKASSMSHLQSLREVKLNNNELETIPNLGPVVSANIT
 LLSLAGNRIVEILPEHLKEFQSLETLDDLSSNNISELQTAFPALQLKYLVLNSNRVTSMEPGY
 FDNLANITLLVLKLNRRNRISAIPPKMKFLPQLQHLELNRNKIKNVDDLTFQGLGALKSLMKOR
 NGVTKLMDGAFWGLSNMEILQLDHNHNLTEITKGWLYGLLMLQELHLSQNAINRISPDWAEFC
 QKLSELDLTFNHLRLDDSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSSLKTLDLKNNNEIS
 WTIEDMNGAFSGLDKLRRLILQGNRIRSIITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
 KLQQLHLNTSSLLCDQLKWLPOWVAENNFQSFVNASCAHPQLLKGRSIFAVSPDGFVCDDF
 PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKDKNELLHDAEMENYAHLLRAQGE
 VMEYTTILRLREVEFASSEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
 RLECAAVGHGPAQIAWQKDGDTFPAARERRRMHVMPEDDVFFIIVDKIEDIGVYSCTAQNSA
 GISISANATLTVLETPSFLRPLLDRTVTVKGETAVLQCIAGGSPPKLNWTKDDSPVLVTERHF
 FAAGNQLLIIIVDSVSDAGKYTCESMNTLGTGRGNVRLSVIPTPTCDSPQMTPASLDDDDGWA
 TVGVVIIAVCCVVGTSVLVWVVIYHTRRRNEDCSITNTDETNPADIPSYLSSQGTLDARQ
 DGVVSSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGPMY
 LKGNVYSGDDPFETYHTGCSPPDRTVLMDHYEBSYIKKKECYPCHSHPSEESCERSFSNISWPS
 HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTGFKALRRPHLDAYS
 SFGQPSDCQPRAFYLKHAHSSPDLDGSGSEEDGKERTDFQEENHICTFKQTLNRYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

[illegible]

CAAAATCTGCGTCCGGCAGAGCGCCGACCTTGACTTGATGGGAGGAGCCCGAGGCCGCGGAGCGAGCTGAGAC
TGGGGAGCGGCTGTGCGCTGTGTGGGCGGCCCTCGCGCGCGGCGCAGCAGAGGAGGGGAAGCTGTGGTCTGCC
CTGCTCCACGAGCGGCACACTGTGTGTAAACGGGAGAGCCCTCGGTGTGTCCGCTGCCATCTCCCTTTTATATA
GAAACTCTTCCACTTGGGAGGCGAGCGCGGAGGAGGAGGCGCTATGTCGTGACGAGGAGCGCGCTGATCTGCAG
GCGCACACAGTCTCCGAGTTTACAGATTTTACAGATTACAAATGGAGCGAGGAGGACGAACAGCTCGTCTGGT
TCCATCAGCCTCTGGCGCGACGGGCACTTGACTTGACGACCCCCCTCAGGACACCAATGGCCCAAGCGGCGTGCTGC
TGCTCTGCTGCTGCTGCGCGCACAGCTGTACCTGGGACTGTGTCTTGGCTGTAGGGCCCCAGGATTTGGCGGAA
TGTGGCGCCACAGCTTGAGCCGAGGAGGAGAAAGAAATTTCCGGAGAGGAGGCGCGTGTGTGATCTAGGCCCTTGAGG
AGCCCGGGCTGGCCACGCCCGGTACAGTGTGCCCGGAGACTGTGCTCTTCCAGAGGGCGTGTGATCACTGTG
GCGGTTATGACTCTGCGTGATTTCCGCGGGGACCTCGCTGAGCACCAACCACTATTCTCTGCAGAAACAACAGG
TGGAAAGATCTACCTCTGGAGGAGCTCTCCGCGTCTGACCGCTGGAGACACTGAACTCGAAAAACAACCGCTGTA
CTTCCGAGGGCTCCAGAGAGGGGCTTTGAGACTTGACCAACTCAATTAATCTGACTTGGCCAAATAACAAGCT
TGACTTTGGACCCCGCTTCTTGCACAAACGCTCTGATAGCTGTGGACTTTGTCTGCAAACTTGCACAAAGATCT
ATGGGCTCACTTTTGGCCAGAGGCAAACTTGTAGGTTGTGTACTCTGCACAAACAAGCTGCGAGACCGCGGGC
TGGCGCAACAATGTTCACAAGCTCGACCAAGCTGAGGTTCTACTCTGTGCAGCAATTTCTCTGCCCACTGTG
CCAAAGCACTCGCCGCGCTGCTTGTACAGAGCTGCACCTCAAGAAACAAGCTTGGAGAAAGATCCCCCGGGGGCCT
TCAGCAGCTGAGCGAGCTTCCGCGAGCTATACCTTCAGAAACAACCTACTTACTGACAGAGGCTTGGAACAACGAA
CCTTCTGGAAAGCTCTCAGCTCTGGAGTACTGTGATCTGTTCAGCAACAACCTTGTCTCGGGTCCAGCTGGGCTCG
CGCGCACTGGCTGTGCTGCTACTTGGAGAAAGAAGCCACTCCGAGGCTGTGAGAGCGAATGTGCTGACCCCACTCC
GAGCTCTGAGTACTGCTGCTGTCAGCAACAACCACTCGGGAGCGAGGCTGACCCCTAGCCCTGGCTCTCCAGGCGC
TCAAGCGTTGCAACAAGGTGTCACTGTGACAAACAACCGCTGGAGCGGCTGCCCACTGCGCTCGCGCGCTG
GACCTCTCATGATCTGCACAAACCAATGTACAGGACTGTGGCGCGAGACTTTGCCACAACCACTTCTCTGGAGG
GGCTCAACTCAGCTACAACCACTGATCCAGCGCAAGGTGCAAGCGAGCTCTTCGCAAGCTCGGCTCTGTGCG
GCTCGTGGAATCTCGGGCTGCACACCGGCTGCACACGCTGCCAACTTGGGCTGCTCGAAATGTCCATGTGCTGAG
TCAAGCGCAATGACTGTGCTGCTTGGCACAGGGGGCGCTGGCGGAGTGTGCTGAGCTGCTGCTGAGCTGACTCTCA
CCAGCAACAACGACTCGCAGCCGAGCCCTCGGCCCTCGCTGCTGGGTGAGCTGCGCACTTGCAGCTGCGACCTGGACA
TCGCGGGAAATCAGCTCACAGAGATCCCCGAGGGGCTCCCGAGTCACTTGAGTACTGTACTCTGCAGCAACAACA
AGATTAGTGGGCTGCCGCTCAACCTGCTTGTGACTCAGCCGCAACCTCAGGGGATTTCTTCTCAGTTTAAACAG
TGCTGTGGGCTCGCGTGTGGAACGCTGCTTCCGAGGCTGAAGCACTTGAGGATTTGGACATTTGAAGAGAGCT
TAGAGTTTGTGTGACATTTCAAGGACCGTGGCCCTTGGGAGAGGAAAGAGGAGGAGGAGGAGGAGGAGGAGG
AGAGGAGGAGAAACAAGTAGTGAAGCGGTGATGTGACATGTGACTAGGATGTGAGCGCCGAGTCTTTTCTGTG
AGCAACGCTTGTGCTGTGAGCGCCCCACTTGCGTGCTTACACAGACACACCACTGCTGACACATGAGGCA
TCCACATCAGCAGGGGCTGACACAGTCTCATATCCCCACCCCTTCGACGCGCTGTCCACGCGCAGACATATGC
ACACACATCAACCTTCAACACCCAGCTGAGCAACAACAACCTTCAACACACAGCTCTGTGTACAC
CCCCACTCAGCGCTGCACGCCCTTGAATCTGACGGGAAAGGCTTGCGCCCTTGCCCTGGCAACAACAGGACAGCA
TTCTCTTCCCCCTGTGACATGTGTATGCGGTATGTCATACACACACAATGCACATGCATGTGTGCGAA
CTCCCTTCCAAAGCTATATGCCACAGACAGCTCTTGCCCGAGCAGATCAGCATAGCATCTGCCGCTCTGCCCT
GTCCATCTGTGCGGTCGGTTCCCTGGAGAGACACAGGATATCATGCTCTGTGGCCAGGTGCTGCCACCTCT
GGAATCAACAAAGCTGGCTTTTATTCCTTTCCATCTATGCGGAGCAGGAGCGCTCAGGACTCTGGGCTGGCT
TGGCCCACTGCTGCTCTCAGGTGCTGGGAGTCACTCTGTAAGATCTCCCTCTGCACGCCCTGTGCGAGGACA
CAGGCACTTTTCAATTTGGGCAACCCAGTGTGGAGCAGGATTTGGAGAGAGCCCTGGGTGTGCTGTGGGCTTGGG
CAGGAGTGAAGCAGGGTGTAGGGGCTGGGCTGAGCGAGGAGGAGGAGGAGCAGGCTGCATCTGTGAGAGACACTTT
GTCTCTCAGGCGCTTGGGGAGGCTTCCGGGCTGCTTTATTTTATTTTATTTTATTTTGAAGGAAAAAATGATAAAAT
CTCAAGCTGATTTTCTGTGTATAGAAAAAATCATATAAAGCAATATCCCTATCCCTGTGCAAAAAAATA

FIGURE 108

MEGEEAEQPAWFHQPWPRGASDSAPPAGTMAQSRVLLLLLLLLLPPQLHLGPVLAVRAPGFGRS
GGHLSLSP EENEFAEEEPVLVLSPEEPGPGPAAVSCPRDCACSQEGVVD CGGIDLREFFPGDLP
EHTNHLSQLNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSSRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSV DANVLTPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCGCGCAGCAGACCTGCTCCGGCCGCGCGCCTCGCCGCTGTCTCTCCGGGAGCGGCAG
CAGTAGCCCGGGCGCGCAGGCTGGGGGTTCCTCGAGACTCTCAGAGGGGGCGCTCCCATCGGCGCCACCACCCC
CAACCTGTTCTCCGCGGCCACTGCGCTCGCCCCAGGACCCGCTGCCAACATGGATTTCCTCTGGCGCTGGT
GCTGGTATCTCGCTCTACCTGCGAGCGGGCCGCGAGTTCGACGCGGAGGTGGCCACGGCAAAATAGTGTCACTGAT
TGCCCTATGTGCTTATGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCGAGTCTGTGGGACAGTGTGACGCC
TGTGTGCCAACCAAGCTGCAACATGGTGAATGTAACGGGCCAAACAGTGAAGTGTATCTCTGGTTATGCTGG
AAAACTGTAAATCAAGATCTAAATGAGTGTGGCTTGAAGCCCCGGCCCTGTGAAGCAGAGTGCATGAACACTTA
CGGCAGCTACAAGTGTCTATGCTCTCAACGGATATATGCTCATGCGCGGATGGTTCTCTGCTCAAGTGCCCTGACCTG
TCCATGGCAAACTGTGATGAGTGGCTGTGATGTTGTAAAGGACAAATACGGTGCCAGTGCCCATCCCTGGCCCT
GCACCTGGCTCTGATGGGAGGACCTGTGTAGATGTTGATGAATGTGCTACAGGAAGAGCTCTCTGGCCCTAGAT
TAGCAATGTGTCAACACTTTTGGGAGCTACACTGCGAAGTGTCAAAAAGCTTCGATCTCATGTATATTGGAGG
CAAATATCAATGTATGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCGAGCAGCTTGTGTCGATGTTATAA
CGTACGTGGGCTCCACAAGTGCAATGTAAAGAAGGATACCGGGTGTGAGCTGACTTGTGTATATATCCCAAA
AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAAGGAAATGGTACCATTTTAAAGGGTGACACAGGAAA
TAAATAITGGATTCTGATGTTGGAAGTACTTGGTGGCTCCGAAGACCATATATTTCTCTCATCATTAACAA
CAGGCTTACTTCTAAGCCAACAACAGACCTACACCAAGCCAACACCAATTTCTACTCCACCACCACCACTAGC
CTTGCCCAACAGAGCTCAGAACACCTCTACCACCTACAACCCAGAAAGGCCAACCCAGGACTGACACTATAGC
ACCGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGAACAACGGGTACAGACAGACCTCAGAAAACCCAGAGG
AGATGTTTTCAGTGTCTGGTACACAGTGTGTAATTTTGACCATGACTTTGTGATGGATCAGGGAGAGAAAGACAA
TGACTTGCACTGGGAACCAATCAGGGACCAGCAGGTGGACAATATCTGACAGTGTGCGCAGCCCAAAGCCCCAGG
GGGAAAAGCTGCAGCTTGGCTGCTACCTCTCGGCGCCTCATGCATTTCAGGGACCTGTGCTGCTCATTCAGGCA
CAAGGTGACGGGGCTGCACCTCTGGCACACTCCAGGTGTTGTGAGAAAACACCGGTGCCACGGAGCAGCTGGTG
GGGAAGAAATGGTGGCCATGGCTGGGGGCAACACAGACTCACTTGCAGGGGGCTGACATCAAGAGCGAATCA
AAGATGATTAAGGGTTGAAAAAAAGATCTATGATGGAAAAATTAAGGAATCGGGATATTAGAGCTTGGAGAAG
AGAAGACTGAGGGGCAACCATTTGATGGTTTTCAAGTATATGAAGGGTTGGCAACAGAGGGTGGCGACCACTG
TCTCTCATATGCACATAAGAATAGAACAGGAACTGGCTTAGACTAGAGTATAAGGGAGCAATTTCTTGGCAGG
TAAAAATTTGTACTACTAGTAGTATGACAGTGAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGG
AGATGTTTTGATATCTATTAAGATGTTTAAAGATGTTCTTACCAGGAAAAAGTACAAATATAGAAATTTCCCAAA
CAITTCCTCTTGACTCTCAATGGAGAGGGATTGAAAGGGGAAGGCCCAACAAATGCTGAGCTCACTGAAATA
TCTCTCTCTTATGGCAATCCTAGCAGTATTAAAGAAAAAGGAACTATTTATTCACAAATGAGAGTATGATGGAC
AGATATTTTGTTCATGGATGATGTTTCAGATTTTTTTTTTTTAAAGAGATCCTTCAAGGAAACAGTTTCAGAGAG
ATTTTCATCGGGTGCAATCTCTCTGCTTGTGTGACAAGTTATCTTGGCTGTGAGAAAGATGCTCCCTGGCCCC
ACACCGGCAGACCTTTCTTCACTCATCAGTATGATTCAAGTTTCTCTTATCAATTTGACCTCTCCAGGTTCCAC
AGAACAGTAATATTTTTTGAACAATAGGTACAATAGAAGGTCTCTGCTCAATTTAACTGTGTAAGAGCGAGGCTGG
AGGGGGAAAAATCAATTAAGCCTTTGAGTAACGGCAGAAATATATGGCTGTAGATCCATTTTAAATGGTTCATT
TCCTTTATGGTCATATACTGCACAGCTGAAGATGAAAGGGGAAAAATAATGAAATTTTACTTTTCGTGACAA
TGATACATTGCATAACTGATGGAAGAGTTATCCAAGTACTGTATAACACTCTGTTTATATTTAATGTTTTT
CTAAAAATAAAATGTTAGTGGTTTTTCAATGGCCTAATAAAAACAATATTTTGTAATAAAAAACACTGTTAGTAAT

FIGURE 110

MDFLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGEICIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCOYGCDVVKGQIRCQCPSPGLHLAPDGRCTCDVDDECATGRASCPFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKNGTILKGDGTGNNNWIPDVGSTWNPCKTPYIPIPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPERPTTGLTTIAPAASTPPGGITVDN
RVQTDQKPRGDDVFSVLVHSCNFDHGLCGWIREKDNLDLHWEPIRDPAGGQYLTVSAAKAPGG
KAARLVLPGLRMLHSGDCLLSFRHKVTGLHSGTLQVVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTGTGCCCTTTAGATTGTGA
AATGTGGCTCAAGGCTCTTCACAACTTTCCTTTCCCTTTGCAACAGGTGCTTGTCTGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTGAGGCCTTACTACCCGCTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGTAGAGACCCCA
CACAATGCCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCCCTGACTTGGAAATACC
AACACAAGTTTACCATGATGCCACCCAATGCATCTCTGCTTATCAACCCCACTGCAGTTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTAGGGAATGGAACCTCTATCTGCCAGTCA
GAAGATACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGACAGATTCACTCCCTCCT
CTGGGCTGTGGAGTATGTGGGAACATGACCTGCATGCCATGTGGAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCACTCCACCTACTCCTTTTC
TCCCCAAAACAATACCTTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCTGTCAAGTGAATGGAAAGTGATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCGTATAAAGGGCTAAAAGTAGGGGAAGTGTCTACTGT
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGCCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCAGAAGACAATGGACTATGTGTCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAATCATTTCACAGTTATCATCACTTCGAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATTTGTACCTTTAGCAAGTATAACTGGAATATCACTATTTTTGATT
ATATCCATGTGCTTCTCTTCTATGGAAAAAATATCAACCTACAAAGTTATAAAAACAGAA
ACTAGAAGGCAGGCCAGAAAACAGAAATACAGGAAAGCTCAAAACATTTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCAGATGTTTCTGGTGTTCAGG
ATTCCAAGCAGGCTGTTCCAGCCTCTGATTGTGTATCGGGCAAGATTGTCACAGTACAGT
GTATGAAGTTATTGACACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACCTTTCATGG
GCTAAACAGTACATTCGAGTGAATTCCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAAGT
ATATTAATCTGGAATCAGTGAAGAAACAGGACCAACACCTCTTACTCATTATTCCTTTACA
TGCAGAAATAGAGGCATTTATGCAAATGAACTGCAGGTTTTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGGAAATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTTTCTCATAAGTTTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTTCATATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAAACTTTACATTGTTGCAATTTTCAGCAGACTTTGTTTTATTAATTTTATTAGTG
TTAAGAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTATTATTGTACAA
CAAAGTAATAAGGATGGTTGTCAAAAAACAAACATATGCCTTCTCTTTTTTTTCAATCACC
AGTAGATTTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAGTCTTATTTTTTA
TTTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTTTTGTCTTTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVGRQALYLPVHYGFHTPASDIQIIWLFRPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTILSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNRPFVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPGYGLQVNSDKGLKVGVEVFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTM DYVCCAYNNIT
GRQDETHFTVITTSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV
YEVIQHHPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

1024205110000

GCAAGCGCGGAAATGCGGCCCTCCGGGAGTCTTGCAGTTCCTTGGCAGTCTCGTGTGTT
GCTTTGGGGTGCTCCCTGGAGCGCAGGGCGGGAGCAGCGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTTGGATGATAGAATTTTATGCCCGTGGTGCCCTGCT
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTTGCTGAATGGGAGAAGATCTTGAGGTTAA
TATTTCGAAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTTTATCATAACTGCTC
TTCCCTACTATTTTATCATTGTAAGAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTTCATAAAGCTTTATAAGTGATAAAGAGTGAAGAGTATTGAGCCCGTTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAAATACCTTTATTGAAGACCTGGATTGCCAGTGTGGGGATCATATACT
GTTTTTGCCTTAGCAACTCTGTTTTCCGGACTGTTATTAGGACTCTGTATGATATTTGTGGC
AGATTGCCTTTGTCTTCAAAAAGGCGCAGACCAGCCATACCCATACCCCTTCAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGCGGATGAAGAA
GATGTTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTTCCACAGAATGC
CATAAGACACACGCTCTCTGGGTCCATCATTTGGCCACAGATAAATCCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTTGATAAAAAACAGAAGATTGATCATTTTGTTTGGTTTGAAGTG
AACTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCTATAAATTGAAGAGTCTA
CATTTCAGAACATAAAAGCACTAGGTATACAAGTTTGAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAATTTTTTGA AAAATCGTGCCAAGCAATAAGATTTATGTATATTTGT
TTAATAATAACCTATTTC AAGTCTGAGTTTTGAAAAATTTACATTTCCCAAGTATTGCATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTCTCATTTGATATAAATTTTCTCTG
TTTCACTGTGTGAAAAAAGAAGATATTTCCCATAAATGGGAAGTTTGCCCATTTGTCTCAAG
AAATGTGTATTTTCAGTGACAATTTCTGTGGTCTTTTAGAGGTATATCCCAAATTTCTTTGT
ATTTTTAGGTTATGCAACTAATAAAAACTACCTTACATTAATTAATTACAGTTTTTCTACACA
TGGAATAACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTTATGTTATTTCTCTGATTC
CAACAAAGTTTGATTTTCTCTGTATTTTCTTACTTACTATGGGTACATTTTTTATTTTTT
CAAATTTGGATGATAATTTCTTGGAACATTTTTTATGTTTTAGTAAACAGTATTTTTTTGTT
GTTTCAAACCTGAAGTTTACTGAGAGATCCATCAAATTGAACAATCTGTTGTAATTTAAAAAT
TTGGCCACTTTTTTCAGATTTTACATCATTTCTGCTGAACCTTCAACTTGAAATTTGTTTTTT
TTTTTTTTTGATGTGAAGGTGAACATTCTGATTTTTTGTCTGATGTGAAAAAGCCTTGGTA
TTTTACATTTTGA AAAATCAAGAAGCTTAATATAAAGTTTGCATTTCTACTAGGAAAAAG
CATCTCTTGTATATGTCTTAAATGTATTTTTTGTCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTTGATGTTTTAAAAATAAATACATTTTATATTTTTTAAAAAGACAA
ACTTCATATTTATCCTGTGTTCTTTCTCTGACTGGTAATATTGTGTGGGATTTCACAGGTAAAA
GTCAGTAGGATGGAACATTTTAGTGTATTTTACTCCTTAAAGAGCTAGAATACATAGTTTT
CACCTTAAAGAAAGGGGAAAAATCATAAATCAATGAATCAACTGACCATTACGTAGTAGAC
AATTTCTGTAATGTCCCCTTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG
TATCGTAATATACAAGTTTTCTTTAAAGCCTCTCCTTTAGAATTTAAAAATTTGTACCATT
AAAGAGTTTGGATGTGTAACTTGTGATGCTTAGAAAAATATCCTAAGCACAAAATAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAA AAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLWGWAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFI~~S~~DK~~E~~WK~~S~~IEPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPSPKLLSESAQPLKKVEEEQEAEDEEDVSE
EAE~~S~~KEGTNKDFPQNAIRQ~~R~~SLG~~P~~SLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.
amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.
amino acids 107-115

N-myristoylation site.
amino acids 20-26, 192-198

Amidation site.
amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTCTGTTAACTAATTCAACAAACGGGACCCCTT
 CTGTGTGCCAGAAACCGCAAGCAGTTGTCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG
 AAGGTCCTGGCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC
 ATTGCTGATGGCCTGGTTTGGTGTCTTGAGCTGTGTGCAGGCCGAATTCTTCACTCTATTG
 GGCACATGACTGACCTGATTTATGACAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
 CTGTGGAGGAAGCCAAAGCTTTCAGATTAAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC
 TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTCTGTGAATGCCTACAAACTGG
 TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTGACAGACTCAGCTGCA
 GGTTTTATCGCCAACCTCTCTGTGCAGCGCAGTTCTTCCCACTGATGAGGACGAGATAGG
 AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATAAGGCTGGACCCAGGCACAATTTCCA
 GAGGGGAACCTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
 GGCCGCTCGGCCTACAATGAAGGGGACTATTATCATACGGTGTGTTGGATGGAGCAGGTGCT
 AAAGCAGCTTGATGCCGGGAGGAGGCCACCAACCAAGTCAACAGTGTGACTACCTCA
 GCTATGCTGTCTTCCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCCTGTCTC
 TCCCTTGACCCAAGCCACGAACGAGCTGGAGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
 GGAAGAGAGAGAAAAACGTTAAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA
 TCTATGAGAGGCGCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGG
 GAGGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTCTCTGTAGGTACCACCATGGCAA
 CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCCGACA
 TCGTCAGGTACTACGATGTCTATGCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
 CCTAAACTTGCACGAGCCACCGTTCTGTATCCCAAGACAGGAGTCCCTCAGTGTGCGCAGCTA
 CCGGTTTCCAAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTTGTGGCCCGAGTAAATC
 GTCGGATGACGATATCAAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAAT
 TATGGAGTGGGAGGACAGTATGAACCGCACTTCGACTTCTTAGGCGACCTTTTGACAGCGG
 CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGATGTAGAAGCTG
 GTGGTGCCACCGTCTTCCCTGATCTGGGGCTGCAATTGGCCCTAAGAAGGGTACAGCTGTG
 TTTCTGGTACAACCTCTTGGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCCCTGCC
 TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCATGAACGAGGACAGGAGTTCT
 TGAGACCTTGTGGATCAACAGAAGTTGACTGACATCTTTCTGTCTCTCCCTTCTCCGTGCT
 CTTACAGCCCATGTCAACGTGACAGACACCTTTGTATGTTCTTTGTATGTTCTATCAGGCT
 GATTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
 GTGACTGAAGTCCCAAGCCCTTCCATTACGCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
 AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCCTTTGTACCTCAGGTGTT
 TTAGGTGTGAGATGTTTCAGTGAACCAAAGTTCTGATACCTGTTTACATGTTTGTTTTAT
 GGCATTTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCTACCAGAAAAA

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FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDVLQDSAGFIANLSVQRQFFP
TDEDEIGAAKALMLRQDTYRLDPGTISRGE LPGTKYQAMLSVDDCFGMGRSAYNEGDIYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLLSLDPSHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVLYLPERDVYESLCRGEVVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEEDWDSPHIVRYDVMSEIEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNRRMQHITGLTVKTAELLQVANYGVGGQYEPHFDFS
RRPFD SGLKTEGNRLATFLNYSMDVEAGGATVFPDLGAAIWPKKGTAVFVYNLLRSGEGDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

Figure 1

SCATGATTATGAGCTTTTACTCTCTCTCTTTTAACTTGGGAAGACAGACAATAATCCCAGTGTGAGTGAATATGATTGT
TCTCATTTTACGCTTTTGGCTGGGGGTAGTTCCGACACCTTCACAGTTTGAGAGCAGGACGAGAGGATGTGTGA
AGACAGGACAATCTCTTGGGGATGCTGTGCTCTTGAGAGCCAGCGGGCTCTCTGTCTTTGGCTCATTTGACC
CAGGTTCTCTGTTTAAATCTGAAGCTCATCTCGGCTGTGTGCCATCAATCATGTTATCTTTAGGCTGTGCC
CTTGGGGACCCACCTTGGCAGGCGCTTACCACCTACCTGAGCTAGAGCTCCCTGTCTGTCTGTCTGGCCGACGCGTCT
CCCTCATCTTAGGGCTGTCTTGGGGTGCAGCTGAGCGCTCTTGGGGTTCTCTGGATCAGCGGGGAGGGAGAA
ATCCCTGTGTGCGAGGCTGTAGGGGAGCGAGGAGGCGCAGAATCCAGATCGAGAGCTCGGCTAGACCAAGAT
ATAGAAGACTTCAAACCCCGGATTTGCTCCCTATCAAGGAGCCCCAACACGCTACAGAGAGTGTCTCAGACTC
GTTACATCCACAGAGAGCTGGGCTCCGTGCGAGCGTGTCTGGTGGTGTCTGCTACCTCCGAGCTACACTGTCCA
CTTTGGCCGTGGCTGTGAACCGTACAGTGGCGGCATCACTCCCTCGGTTACTCTATCTACGCGGACGCGGGGG
CCGGGGCTGACGAGGATGTCAGTGTGTGTCTCATGGGATAGCGGCGGCTGTGCTCATGTGACAGACACCTGC
GCCACTCTTACACACATCTTTGGGGCCGACATACGACTGTGTTCTCATCATCGAGGATGACACATATGTGACGGCC
CCCGCTGGCAGCCCTTGTCTGGCCACTCAGACTCAACCAAGACTGTACTTAGGCGGAGGACGAGAGTTCATTG
GCGCAGGCGAGCAGCGGCGGTACTGTCTAGGGGGTCTTGGCTACTCTGTTGACATCGAGTCTCTGCTCTCTGTG
GGCCACTCTGATGCTGCTGCGAGAGACATCTCAGTGGCCGTCTGACAGTGGCTTGGACGCTGCTCATCTG
ACTCTTGGGCGCTGCGCTGTGTTCTACAGACAGGGGACGAGCTGCTCATCTTCAAGTGGCCAAATATGGG
ACCTTGAGAGGAAGAGGACTCGGCTTCTCTGAGTGGCTCAGGCTGACGCTTGTCTGGAAGGTTACCCCTATGT
ACCGGCTCCACAAACGCTTACGCGCTCTGAGATGTGAGAGCGGGCTTACAGTGAATAGAGCAAACTGCAGGCTCAGA
TCCGAAGCTGACCGTCTGACGCCCGAAGGGGAGCGAGGCTCAGAGCTGGCCCTTGGCTCTCCCTCTCTTTCA
TACCACATCTCTGCTCTTGAGGTGCTGAGCTGGGACTACTTCAAGAGCTGACAGCTCAACCTTCTCTGTGAGATAGGG
CTTCCAGTGTCCCACTACAGSGGCTAGCAGGGCGACGTGGTGTATGCTTGTGAGACGTGCCCTGAGGACGCTCA
ATCGGCGCTATACGCCCCCTCTGCGTCTCAGAAACGACGACTGTCTGAGACAGCGTGGGACCGGGGCCCTGCGTGC
GGGTGAGCTGCTGTGGCCACTGAGCGGGGTGGAAATCTGACTATGCCCATTGTCACTGAGGCGACCCGAGTGC
ACTGTGCTGCGACTCTGTGTTGGTGGAGTGTGACGCCCCGCTTCTCTCGAGGCGTCTGACGCAAAATCTG
TGAGGCGACGAGAACATCTGATGCTCACTCTGTGTGGTCTACGGGCGACGAGAAGGTGGCGTGGAGCTCCAG
ACCCATTTCTTGGGGTGAAGCTCGACGACGGAGATTAGAGGACAGGTTCTCCAGTGGACGAGGCTGGCTGTGCTCT
CTGTGCGAGACGAGGCTCTCCAGAGTGCAGCTCATGAGCTGGTCTCGAAGAGACGCTTGTGGAACATCTCT
TCTTCTTCAACCCGTGTGGAACAGGCGCTGGGCGGAGTCTCAACCGCTGTGCGATGAATGCCATCTGTGGCT
GGCAGGCTCTTCTCAGTCACTTTCAGAGATTTCAATCTGCGCTTGTCAACACAGAGATCAACCCAGGCGCCC
CGGGGGCTGGCCCTGACACCCCTTCTCTGTTGCTGACCCCTCCGGGGGGGCTCTTACGGGGGGAGATGAT
ACCGCGAGCTTCTCGGAGAGGCTGTTCTTCAACAGCTGACTACTCTGGCGGCGGAGCGCGGCTGGCAGTGAAT
TGACGAGCCGAGGAAGAGGAGGAGCCCTGGAGGGCTGGAGTGTATGATGTTTCTCTCCGTTCTCAGGGTCT
ACCTCTTTCGGCGGCTAGAGCGAGGCGTGGTGTGAGAAGTTCTCTCTCGAGACTCGACGCTCAGGCTCAGTGA
AACTCTACCCACGCTGCGCCTCTAGCAACCTCGAGGGGGGAGGGGCGTCCGACAGCTGCTATGCTCTCTTGA
ACGAGGAGCGAGGCAATAGCACTTACCGCGCTGGGGGCGCTAACTCATTAATCTTCTTGTCTGCTCGCC
CAGGAAGGGCAGGCAAGATGGTGGACAGATAGAGAATTTCTGCTGATTTTTTTAAATATGAAATTTATTAA
ACATGTTCTCTGCC

FIGURE 118

MRLSSLLALLRPAFLILGLSLGCSLLLRVSWIQGEGEDPCVEAVGERGGPQNPDSSRARLD
QSDDEDFKPRIVPYRDPNPKPYKKVLRTRYIQTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTHFGADYDWWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWPVGLPAPFTPHSRFEV
LGWDYFTEQHTFCADGAPKCPLOGASRADVGDALETALEQLNRRYQPRLRFOQRLLNGYR
RFPDPARGMEYTLDLLLECVTQRGHRRALARVSLLRPLSRVEILPMFYVTEATRVQLVPLLL
VAEAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTVWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPPGAGDPSPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEEALEGLEVMVDVFLRFSGHLHFRAVEPGLVQKFSRLRDCSPRLSEELYHR
CRLSNLEGLGGRAQLAMALFEQEQA NST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGTCTTCTGTCCCCAAGCC
GTTCTAGACGCGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTTCGAGTATACTGTATTATCCTTGTAAAAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTTCAGTCAATTAATATGGACACAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTTGATAAGTATAGAGACCAATACAACTG
GTTCTTCCTTGCACGCCCCACTACGTTTGCTATCATTTGAAAACCTAAAGTATTTTTGTAA
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGCTTAAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGCTCTGAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTTGCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAATCTGTTGGGCTTCTATTAAAGAGGCAATGACTTATCACCC
CAACCAGGTAGTAGAAGGCTGTTGTTGAGATATGGCTGTACTTTTAAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGGTATACCGCCTTAGGGCATTTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGTTCTGACAATGACTTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCAATTATTTGTAGTAGTAACATACATATCCAA
TACAGCTGTATGTTCTTTTCTTTTCTAATTTGGTGGCACTGGTATAACACACATTAAAG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTAAAAACATGAACATTGTAAATG
TGTTGGAAGAAGTGTTTAAGAATAATAATTTGCAAATAAACTATTAATAAATATTATAT
GTGATAAATCTAAATTATGAACATTAGAAATCTGTGGGGCACAATTTTTGTCTGATTGGTT
AAAAAATTTTAAACAGTGCTTTAGCGTTC TAAGATATGCAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTTCCTCTCAAATGTACAATAAGCACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFVYCIILVKPKDVS LWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAI IENLKYFL LKDPSPFPYLGHTIKSGDLEYVGM EGG
IVLSVESMKRLNSLLNIPEKCP EQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDV FNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAF GHI FNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

COLUMBIA

[illegible]

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSPFWDVGEPNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

[illegible]

SGGATCTACAAAGCCGGCGCTCGCTCGCCGTGCCCTCTCAGCAACCCCTGCATATGCGCGCTGAGAGCGGCACCGCGACG
 TCGCGCTTCGCGCTCGCGCTCGTACTGCTACTGCTGCTGCTGCTTTGAGAGCTGCGCTGATAGGGCGCTGTAAATCT
 TCAAAATCCAGCAATTCGAACCCCACTGGATACAGGAATTTGAAAGTTTGGGAAGCTGCTTGTGCATATTCAGGATTCGCG
 AGCAAGTGCACCCAGGATCCAGTTCAGTGGTGAAGAAATATCGAGATGAACAAACCATATGTGTTTGTGACACAAAA
 TTCAGGGGAGCTTGCGCGGGTCTGCGAGAAATCTGGGGAAGCAATCCCTGAAGATCTTGAATGTGACACGGAGAG
 ACTCGACCTTTATTCGCTGTGAGGTCTGTGCTCGAAATTTGCGACCAAGGAAATTGATGAGATTGATGTACAGTTAA
 CTGTGCAAGTGAAGCAGTACGACCTCTGTGTAGATGTGCGAAGGCTGTACAGGTAGTGAAGTACGATGGGCAACTCG
 ACTGCGACGAGAGTGGAGGCGCAACCCCGCCCTACATCAGCTGTGATTCGCAATGATGTACCACTGCCACGGATAT
 CCGAGGCGAAATCCGAAATTTGCGAATTTCTTTCTTCCATTTAAACTCTGAAACAGGCACTTTTGGTGTGTCTACTGCTG
 TTTCAAGAGCGACGCTTGGGAGCACTATCTGCAATTCGTTTTCAGTACGCGAGGCTACGCGAGTTGTGGAGGACGAG
 AGATGGGAAGTCTATGACCTTGAATCTTGGCGAAATTTGGGCGGGTCTTGTGTTGTCTGCTGTACTCGGCGCTGA
 TCACCTTTGGGCACTGCTGTGCATACAGAGCGCTGAGTACTTCATCAACATAACAGGATGGAGAAAGTTACAAGA
 ACCGAGGGAACCAAGATGTAGTCTAACTACATCCGCACTGACGAGGAGGGCGCACTTACAGACAAGTCACTGTTGTT
 TGATCTGAGACCGCGCGGTGTGCTGTGAGAGCGCACAGAGCGCAGCTGCGACATACCTGTCTGTAAGAACTCTGCTCAA
 GCGACGAGGCGTGTGACTGACTCGACAGCGATGACACTTTCGAAGCTTTTTCGTTTGTGGCCAAAGTTGACCA
 CTACTCTTCTTACTTAAACGCCATCAATGATAGTAAATTTCTTCAAGTGGACCCGGGTAAATTAACCAACAA
 GGAAGCGAAATCGGTTGCGTTTCACTGAGTTGGGTTTCTGAAATCTGTCTTGGCTGCTTCCGCAATGATTTAGG
 GTGATCTTAAAGAGTTTGTCTACGCTTAAACCGCCGTGCTGGCCGCTGTGAAGCGCAGCATGTCTACCACTGTGCTGT
 CAGAGCCGACACAGCAGCATGTGATGATGCGAGGCTGTGGCGACAGCAGCAGCGCATCTCCGCGGGAAACCA
 GAAAGGGTCTTTACACAGCAGCTTACTCTATCGCGCCACAGACACCCGAGTTCTCTTCTTAAAGCTCTGCT
 TGATCGTGTGTGACGTCTGCTGTGAGAGAGCTTTTGGATCAGATTTTGTAAAAACCAAAATCAGGAAG
 GTAAATTTGCTTCTGGAAGAGGATCTTGCCTAGCAACCTGCTTCTTCCAAGGCTGTGAGATTTAAGGAA
 ACTAATTTGCTTTAGCTTAAGTCTTGTGAATGCTGCTAGAAATGCTTTCTTCTTGGCTGTTGTTTATTTATAAAT
 TACATCTAAATTTTGTCTAAGGATGTTTGTGATTTTGAATAAGAAATTTCTATTTTAAATCTAAATATTGAT
 TACAAGTCTTAAATTAACCTTTTAAAAAGCTTCAACTCTTGTGAAGTTTCAAGTCTACTAGTTGTAAAT
 TCGAAATATCAATAATTAGAGTATTTTACCAAGGAATCCCTCATGGAAGTTTCACTGTGATGTTCTTTCTTCT
 CACACAAGTTTGTAGCTTTTTCACAAAGGAATCTACATCTGTCTACATCAGACAGCATGTGCTTGAAGAACCTT
 TAAAAATTCAGTTAAGCAATTTGAAATAGTTTGTGATCTTTCTTAAAAAGAACTCTCAGGTTAGCTTTGAACT
 GCTCTTCTCTGAGATGATGACGACAGCTCTCCGCCAGAGGCGCCACGAAAGCCCTCAGATGTATACATACAGATG
 CAGTACGCTTCTGGGTTTGGCGCAGGCGCTCGACCTCTAGCTCATGTGCTGCTGTGTCGACAGAGGCGCTC
 GCATCTTTTGGCCCTGGCAGTGGCTGTGCTCCAGTGAAGCTTTACTACATGGCCCTTGCTCTATCCAGCACAGCT
 TCTCAGGTGGGCACTCGAGGACACTGGTGTGTTCCATGTAGCTTTCAGTGTGGCCCTTGCTCTATCCAGCACAGCT
 TTTTGGTATGTAGGTGCTCGACAAATATGGGCGCCCAAGTGCTATTTTCTTTTAAAGTTTGTAAATTTTGTGTT
 AGATGTTGTCAAGGCGCAAAGGCAATTTGCGAATCAAGTCTGTCAAGTACATAACATTTTAAAAAGAAATGAT
 CCGATCTGTTCTCTTCTTGGCACAGAGAAGACCCAGAGCGACAGGCTCTGTGCAATTTTCAAAACAAACATGAT
 GAGTGGGCGGCGCAGTGCACGCTTTTAAAGAAAGCTCAGGTGGAGCAGCGAGTGAAGGCTCGGGCGGGAGGAAG
 TGAACAGCTGTAATCAAAAGAGTTTCTAAATTTTGACTTTTAAATTTTATCTCGCCGGAGACATGCTCCCATTT
 TGTGGGGGACATPAGCAACATCTACGAGAGGCTGTGTTCTTCAAGAGCGAGTTGTTCTCAGCTCAGCTGCGCT
 GCGGTGCTGGAATCAGCACTGAGGTTCTGTGTAAGACAGAGGATGCTGTGAAGAGGAGCACTCCACTGTGCTCGGA
 GAATGGCTCTCACTACTCACTCTGTGCTTCAAGCTTCAAGTGTCTTGGGTTTGTATCTTTACACTGTGACGTTTCTT
 AATGTGATACATGAGACTGTGTTGACTTTTGTAGTATGTGTGAACACTTTGGCGCAGGCGCCCTGGCAGAGGCA
 GAAATTTGCTCCAGCATGTGGCTCAGTGTCTCCGTGGTGTGCTGCTGCAATGGCATCTTGGATGCTTAGCATGAGATT
 CCTCCATCACTGGCACTCTGTGAGAGAGGAGGTGGCTCCCAACCTCAGCTTGTGGGATTTCAAGCTCAGCTGCTCT
 TCTTGGTTGTGATAGTATGATGAGTTAGCTTTATGTGCCCCCTTCTTATACGTTAAACAACTTTACACTAGTGGCA
 TGGGAACAGGCTGTAAAGAAATGAGAGAGAGTGAAGTGAAGTCTGGGAAGTGGCTGCTATACATGAGACTAGA
 CGGAAAGGAAATCTCGTATTTTAAATATGAAATGTACTCAAGTACAGGCGGATACAGAGGCTGATTTCT
 GCTTTTGGATGATGTTGCTGTACACAGTGCTACAGACTTGTACTAAACACCGTAATTTGGCATTTGTTTAACT
 CTCATTTATAAAGCTTTCAAAAGAACCA

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTFVVQEFESVELSCIITDSQTS
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVTRRDSALYRCEVVARNDR
EIDEIVIELTVQVKPVPVCRVPKAVPVGKMATLHCQSESGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSSFLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEYVDLNIIGGIIG
VLVVLAVLALITLGICCAAYRGGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267